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Attach #22

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SEP 28 2000

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SEQUENCE LISTING

<110> Lowery E., David
Fuller E., Troy
Kennedy J., Michael

<120> Anti-Bacterial Vaccine Compositions

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<151> 1999-09-10

<150> 60/128,689

<151> 1999-04-09

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ttttcataaa tatcaataaa ggattagtt atg gca gca gag ctt aca aca gcg 233

Met Ala Ala Glu Leu Thr Thr Ala
1 5

gga tat att ggg cac cat tta gca ttc ttg aaa aca ggg gat tct ttc 281

Gly Tyr Ile Gly His His Leu Ala Phe Leu Lys Thr Gly Asp Ser Phe
10 15 20

tgg cat gtt cat tta gat acc ctt cta ttt tca att att tca ggt gca 329

Trp His Val His Leu Asp Thr Leu Leu Phe Ser Ile Ile Ser Gly Ala
25 30 35 40

att ttt ctt ttt gtt ttt tca aaa gtt gca aaa aaa gca acg ccg ggt 377

Ile Phe Leu Phe Val Phe Ser Lys Val Ala Lys Lys Ala Thr Pro Gly
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gtg cct agc aag atg caa tgt ttt gtt gag ata atg gtt gat tgg att	425
Val Pro Ser Lys Met Gln Cys Phe Val Glu Ile Met Val Asp Trp Ile	
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Asp Gly Ile Val Lys Glu Asn Phe His Gly Pro Arg His Ala Val Gly	
75 80 85	
cca tta gca tta act att ttc tgc tgg gta ttc att atg aat gct atc	521
Pro Leu Ala Leu Thr Ile Phe Cys Trp Val Phe Ile Met Asn Ala Ile	
90 95 100	
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Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly	
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att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta	617
Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu	
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ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa	665
Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys	
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Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe	
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Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr	
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Tyr Ala Gly Glu Leu Ile Phe Ile Leu Ile Ala Val Met Tyr Met Ala	
205 210 215	
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Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp	
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Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met	
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Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His	
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Val Ala Lys Lys Ala Thr Pro Gly Val Pro Ser Lys Met Gln Cys Phe
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Val Glu Ile Met Val Asp Trp Ile Asp Gly Ile Val Lys Glu Asn Phe
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His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys
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Trp Val Phe Ile Met Asn Ala Ile Asp Leu Ile Pro Val Asp Phe Leu
100 105 110

Pro Gln Leu Ala His Leu Phe Gly Ile Glu Tyr Leu Arg Ala Val Pro
115 120 125

Thr Ala Asp Ile Ser Gly Thr Leu Gly Leu Ser Ile Gly Val Phe Phe
130 135 140

Leu Ile Ile Phe Tyr Thr Ile Lys Ser Lys Gly Met Ser Gly Phe Val
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Lys Glu Tyr Thr Leu His Pro Phe Asn His Pro Leu Leu Ile Pro Val
165 170 175

Asn Leu Ala Leu Glu Ser Val Thr Leu Leu Ala Lys Pro Val Ser Leu
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Ala Phe Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile
195 200 205

Leu Ile Ala Val Met Tyr Met Ala Asn Asn Phe Ala Leu Asn Ser Met
210 215 220

Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile
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Thr Leu Gln Ala Phe Ile Phe Met Met Leu Thr Val Val Tyr Leu Ser
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aaa atg gca ggt gct aaa gag ata aga acc aaa atc gcg agt gta aaa 408
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agt aca caa aaa att act aaa gcg atg gaa atg gtt gct gcc tcg aaa 456
Ser Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys
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atg cgt aaa acg caa gaa cgc atg tct tct tca cgc cct tat tca gaa 504
Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu
35 40 45

aca ata cgt aac gtg att agc cac gtt tcc aaa gca acg att ggt tac 552
Thr Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr
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aag cat cca ttt tta gtg gat cgc gaa gta aaa aaa gtg ggc atg att 600
Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile
65 70 75

gtt gtg tcc aca gat cgt ggt ctt tgt ggt ggc tta aac gtg aac ttg 648
Val Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu
80 85 90 95

ttt aaa act gta tta aat gaa atg aaa gaa tgg aaa gaa aaa gat gtt 696
Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
100 105 110

tcc gtt caa ttg agt tta atc ggt tct aaa tct atc aac ttt ttc caa 744
Ser Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln
115 120 125

tct ttg gga att aaa att tta acc caa gat tca ggt att ggt gat act 792
Ser Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr
130 135 140

ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct 840
Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala
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Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe
160 165 170 175

att aac acg atg tcg caa aag cca gta ttg gaa aaa tta att cca tta 936
Ile Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu
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Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val
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cgt tat tta gaa tct cag gtt tat caa gca gca gtt gaa aac ctt gct 1080
Arg Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala
      225                230                235

tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac 1128
Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn
      240                245                250                255

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Ala Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg
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caa gca agt att aca aat gaa tta aat gaa att gtt gcc ggt gca gca 1224
Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala
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His	Pro	Phe	Leu	Val	Asp	Arg	Glu	Val	Lys	Lys	Val	Gly	Met	Ile	Val
65					70					75					80
Val	Ser	Thr	Asp	Arg	Gly	Leu	Cys	Gly	Gly	Leu	Asn	Val	Asn	Leu	Phe
				85					90					95	
Lys	Thr	Val	Leu	Asn	Glu	Met	Lys	Glu	Trp	Lys	Glu	Lys	Asp	Val	Ser
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Val	Gln	Leu	Ser	Leu	Ile	Gly	Ser	Lys	Ser	Ile	Asn	Phe	Phe	Gln	Ser
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Leu	Gly	Ile	Lys	Ile	Leu	Thr	Gln	Asp	Ser	Gly	Ile	Gly	Asp	Thr	Pro
130						135					140				
Ser	Val	Glu	Gln	Leu	Ile	Gly	Ser	Val	Asn	Ser	Met	Ile	Asp	Ala	Tyr
145					150					155					160
Lys	Lys	Gly	Glu	Val	Asp	Val	Val	Tyr	Leu	Val	Tyr	Asn	Lys	Phe	Ile
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Asn	Thr	Met	Ser	Gln	Lys	Pro	Val	Leu	Glu	Lys	Leu	Ile	Pro	Leu	Pro
		180						185					190		
Glu	Leu	Asp	Asn	Asp	Glu	Leu	Gly	Glu	Arg	Lys	Gln	Val	Trp	Asp	Tyr
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Tyr	Leu	Glu	Ser	Gln	Val	Tyr	Gln	Ala	Ala	Val	Glu	Asn	Leu	Ala	Ser
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Glu	Gln	Ala	Ala	Arg	Met	Val	Ala	Met	Lys	Ala	Ala	Thr	Asp	Asn	Ala
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OCT 18 2000

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 Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala
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aat gtc tta gaa gcc gcc atc caa aac cag ata aaa cgc gtc gtc tgt 144
 Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys
 35 40 45

ctt agc aca gat aaa gcg gtg tac cca att aat gcg atg ggc att tct 192
 Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
 50 55 60

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 Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
 65 70 75 80

ggc aca cca acg aca atc tgt tgt act cgc tat ggc aat gtc atg gca 288
 Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
 85 90 95

tcg cgt ggt tcg gtt atc cca tta ttt gtc gat caa ata cgt caa ggc 336
 Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
 100 105 110

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 Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
 115 120 125

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 130 135 140

aat ggt gat gtt ttt gta caa aaa gcc ccc gca gca acc att ggt acc 480
 Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
 145 150 155 160

ctt gcc aaa gca att acc gaa tta tta tct gtc cca aat cac cct att 528
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 165 170 175

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 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
 195 200 205

atc cca gcc gat caa cgc agt tta aat tac agt aaa tat gtc gaa aaa 672
 Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
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Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
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Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
          100             105             110

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Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
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Val His Ile Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys
    30                   35                   40                   45

act tta gct caa gca ccg tat aac acc gag att caa tgg aaa aat ttg 4214
Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu
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His Phe Trp Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu
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Pro Ala Glu Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser	
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Trp Tyr Leu Asp Lys Asp Ala Ala Lys Leu Leu	
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 35 40 45
 Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu His Phe Trp
 50 55 60
 Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu Ser Asn Tyr
 65 70 75 80
 Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile Pro Ala Glu
 85 90 95
 Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser Glu Leu His
 100 105 110
 Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln Val Phe Asp
 115 120 125
 Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala Ser Leu Phe
 130 135 140
 Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val Ile Ala Lys
 145 150 155 160
 His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala Lys Leu Ile
 165 170 175

Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser Ser Lys Ala
 180 185 190

Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln Leu Pro Tyr
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Asp Lys Asp Ala Ala Lys Leu Leu
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Pro Phe Phe Asp Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu
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cct ttg cct att cat caa ctc gat gat gaa acg ctg gat aat ttc tat 1766
Pro Leu Pro Ile His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr
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ccc gac aat aat tta ttg ttg ctc aat tcg cta cgc aaa aat ttt act 1814
Pro Asp Asn Asn Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr
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Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
65 70 75
aaa agt cac ctc tta aaa ggc att act cat cat ttt ttc ctt tta cag 1910
Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
80 85 90
cgc ccc gct atc tat gtg ccc tta gaa aaa tcc caa tat ttc tca ccg 1958
Arg Pro Ala Ile Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro
95 100 105
gcg gta ctc gaa aac tta gaa caa caa caa ttg gtt tgt tta gat aat 2006
Ala Val Leu Glu Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn
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125 130 135 140
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Leu Phe Asn Arg Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser
145 150 155
gca aat caa tcc cca act gca tta cct gta agt tta cct gac tta gct 2150
Ala Asn Gln Ser Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala
160 165 170
tca cgt tta cgc tgg gga gaa agc tat cag ctg gtc ccc tta aat gat 2198
Ser Arg Leu Arg Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp
175 180 185

caa caa aaa atc cat gta ttg caa aaa aat gca cat caa cgt ggt atc 2246
Gln Gln Lys Ile His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile
190 195 200

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205 210 215 220

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Asp Met Lys Thr Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser
225 230 235

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<213> Pasteurella multocida

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His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn
35 40 45

Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln
50 55 60

Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly Lys Ser His Leu
65 70 75 80

Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln Arg Pro Ala Ile
85 90 95

Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu
100 105 110

Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn Leu Gln Ala Ile
115 120 125

Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg
130 135 140

Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser Ala Asn Gln Ser
145 150 155 160

Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg
165 170 175

Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile
180 185 190

His	Val	Leu	Gln	Lys	Asn	Ala	His	Gln	Arg	Gly	Ile	Glu	Leu	Pro	Asp
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Leu	Phe	Glu	Ala	Leu	Ser	Lys	Leu	Asp	Lys	Ala	Ser	Leu	Gln	Ala	Gln
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Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys	
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Ile Tyr Glu Arg Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu	
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Gly Leu Leu Tyr Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu	
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Phe Leu Pro Ser Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly	
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Phe Ser Met Val Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu	
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Leu Leu Ala Leu Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys	
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Gln Arg Arg Leu Phe His	
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 35 40 45
 Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu Gly Leu Leu Tyr
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 Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu Ile Gly Leu Ser
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 Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His Leu Asp Leu Gln
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 Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu Phe Leu Pro Ser
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 Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Leu Ala Leu
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35 40 45
Ile His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser
50 55 60
Thr Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile
65 70 75 80
Gly Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile
85 90 95

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 Glu. Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu
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 Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr
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 gtt cat act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg 728
 Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val
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Gln	Glu	Gln	Asp	Lys	Thr	Asp	Ile	Lys	Val	Val	Lys	Met	Gly	Ala	Ile	
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Met	Tyr	Tyr	Gln	Pro	Leu	Thr	Arg	Tyr	Ile	Trp	Thr	Pro	Leu	Ser	Gly	
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Asn	Ala	Ser	Arg	Glu	Phe	Asn	Asn	Leu	Glu	Ser	Phe	Leu	Asp	Ala	Leu	
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Phe	Gly	Ser	Thr	Thr	Ile	Leu	Lys	Ser	Ser	Phe	Tyr	Ser	Thr	Glu	Asn	
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Phe	Ser	Ala	Tyr	Gln	Leu	Leu	Ser	His	Ile	Gln	His	Ser	Pro	Met	Tyr	
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caa	aaa	gcg	atg	gca	caa	gtg	ttt	ggg	gca	gag	tgg	cat	agt	aaa	tcc	1304
Gln	Lys	Ala	Met	Ala	Gln	Val	Phe	Gly	Ala	Glu	Trp	His	Ser	Lys	Ser	
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Tyr	Asp	Glu	Met	Arg	Asn	Lys	Trp	Lys	Ser	Phe	Lys	Glu	Asn	Pro	Thr	
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Leu	Glu	Gly	Lys	Leu	Thr	Thr	Leu	Gln	Asn	Gly	Glu	Tyr	Ala	Glu	Arg	
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Gly	Lys	Phe	Asp	Glu	Ser	Ile	Gln	Ile	Gly	Lys	His	Gln	Leu	Ser	Leu	
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Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu	
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Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly	
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485 490 495	
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Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys	
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Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys	
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Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu	
565 570 575	

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Asn Asp Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu	
870 875 880	
ggg cat tta cat ctt gaa aca gat aag gat tca act att gat gta caa	3224
Gly His Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln	
885 890 895	
gca tcg gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg	3272
Ala Ser Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val	
900 905 910	
aat ctc aaa aat aca tac aat act aaa cat gcc tac cgt gag aaa ttc	3320
Asn Leu Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe	
915 920 925	
tcg ccg agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa	3368
Ser Pro Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys	
930 935 940 945	
gtc cca ctt tta ggc gtg tcg tct cca tcc agt tat tca gag cat act	3416
Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His Thr	
950 955 960	
agt gag gca act tca gag gga tca atc ttc gaa gta ggg cac tta cat	3464
Ser Glu Ala Thr Ser Glu Gly Ser Ile Phe Glu Val Gly His Leu His	
965 970 975	
ctt gcg gta gac aga gat gtg aac caa gcg ggg agt aaa att aag gct	3512
Leu Ala Val Asp Arg Asp Val Asn Gln Ala Gly Ser Lys Ile Lys Ala	
980 985 990	
aag tat acc act ggt gtt gtg aaa ggg aac ttt aat act gaa gcg ggc	3560
Lys Tyr Thr Thr Gly Val Val Lys Gly Asn Phe Asn Thr Glu Ala Gly	
995 1000 1005	
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Lys Asn Ile Lys His Val Glu Lys Glu Glu Tyr Ser Ser Gln Leu Phe	
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gct tca gca cac gcg agt ggt ggt ggc acc tca gtt cgt tat gac tat	3656
Ala Ser Ala His Ala Ser Gly Gly Gly Thr Ser Val Arg Tyr Asp Tyr	
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Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn His	
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Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys Asp	
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Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys His	
1075 1080 1085	

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Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp Ile	
1090 1095 1100 1105	
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Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu Ile	
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Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val Ala	
1125 1130 1135	
caa gct caa tca aat gcc aat aag gat aag gaa aat aaa gcc cca gaa	3992
Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro Glu	
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ata aaa gaa tta tca gag gct gaa atc gcg gat ctc atg tca gaa aaa	4040
Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu Lys	
1155 1160 1165	
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Ser Lys Ala Tyr Phe Asp Asp Phe Ala Glu Gln Ala Lys Lys Ala Pro	
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Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser Lys	
1190 1195 1200	
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Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys Val	
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Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser His	
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Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp Gly	
1235 1240 1245	
aca gta gca tta caa cat gct agt gat gtc tta aat att gtg acg ggg	4328
Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr Gly	
1250 1255 1260 1265	
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Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His Glu	
1270 1275 1280	
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Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly Gly	
1285 1290 1295	
aat gtc aca ctg tca gca cgc agt ggt agt gtg aac ctt aaa aat gta	4472
Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn Val	
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Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp Val	
1315 1320 1325	
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Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val Ser	
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Arg Gln Lys Leu Ser His Gly Val Asn Ala Gly Cys Ser Met Met Ser	
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Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu Ser	
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Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys Ala	
1380 1385 1390	
cgc aac atg aaa gtt gaa gca ggt cgc gat ttt aat gtt gtc agt tcg	4760
Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser Ser	
1395 1400 1405	
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Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr Asn	
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Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val Asp	
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Tyr Asn Leu Ser Ala Gly Val Ala Leu Ser Ser Ala Thr Ile Ala Thr	
1445 1450 1455	
cca acc ggt aat gtt ggt ttc ggt tat acc aat gag acc gaa agc aag	4952
Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser Lys	
1460 1465 1470	
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Arg Thr Val Asn Gln Gln Ala Gly Ile Lys Ala Asn Lys Ile Thr Gly	
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Gln Thr His Asp Leu Asn Leu Glu Gly Gly Tyr Leu Val Ser Asn Asp	
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Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala Leu	
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His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val Gly	
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Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg Ala	
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Glu Gln Lys His Tyr Asn Ala Thr Gln Lys Ser Thr Leu Ser Gly Val	
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Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu Thr	
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Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln Phe	
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Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys Asn	
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Lys Leu Ser Ala Pro Asn Asn Asp Thr Asp Met Ala Ser Gly Ser Thr	
1620 1625 1630	
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Leu Arg Ser Arg Ser Thr Thr Glu Glu Ala Asp Val Pro Thr Thr Arg	
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tcg cgt gta acg gat gag gcg gat tct gta tcc gtg aaa aat ccg att	5528
Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro Ile	
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Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn Val	
1670 1675 1680	
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Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr Thr	
1685 1690 1695	
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Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser Lys	
1700 1705 1710	
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Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr Ser	
1715 1720 1725	
gat gag cat ctt tat gca gag att aat gaa cca aca tat agc cgt gtt	5768
Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg Val	
1730 1735 1740 1745	
ggt gat aaa aat gca gat atg aga cgt cat aac gcg gca ggt aca aca	5816
Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr Thr	
1750 1755 1760	
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Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp Pro	
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Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp Gly	
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Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr Lys	
1795 1800 1805	
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Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn Ala	
1810 1815 1820 1825	
ggt aac ttg ata ggg caa aat ggc tta ggc agc att tat cac agc cca	6056
Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser Pro	
1830 1835 1840	
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Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn Lys	
1845 1850 1855	

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cgc cat acc tta gat aaa tca aga tta ttt tat aac gca cat aat aaa Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn Lys 1890 1895 1900 1905	6248
acc tta ttt agc gtg cct atc gtt gat gca aaa gtc aaa atg ctg ttt Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu Phe 1910 1915 1920	6296
gct gaa aaa aat atc caa gtc aat tac gat cgt agc ctt aca gcc att Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala Ile 1925 1930 1935	6344
gat ctg agt aaa cgt att gcg acc ttt aat agc cca gaa gga gtt gta Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val Val 1940 1945 1950	6392
gaa gtc cct tat gat ttt att aat gtg gta cct cca atg cga gca cct Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala Pro 1955 1960 1965	6440
gat gcc gtt cgt caa tca gca ctc gcg tgg caa gaa gga aaa tgg gct Asp Ala Val Arg Gln Ser Ala Leu Ala Trp Gln Glu Gly Lys Trp Ala 1970 1975 1980 1985	6488
aac gat ggt tgg gtt gaa gta gaa aaa cat acc ttg cgt cac cgt cgt Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg Arg 1990 1995 2000	6536
tat gcc aat gtg ttt gct gtg ggt gat gtg gca ggg gtc cca aaa ggc Tyr Ala Asn Val Phe Ala Val Gly Asp Val Ala Gly Val Pro Lys Gly 2005 2010 2015	6584
aaa acg gct gcc agt gtc aaa tgg caa gtt cct gtt gca gtg gca cat Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala His 2020 2025 2030	6632
tta ctc gca gaa tta gag ggc aaa cct tgt gat gaa att tac aac ggt Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn Gly 2035 2040 2045	6680
tat aca tct tgt cca tta att act caa tta gga aag ggg atg cta gta Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu Val 2050 2055 2060 2065	6728
gaa ttt gat tat aac aac cac tta aca cct tct ttc ccc ggt gta ata Glu Phe Asp Tyr Asn Asn His Leu Thr Pro Ser Phe Pro Gly Val Ile 2070 2075 2080	6776
gcg cca tta gaa gaa ctg tgg gca aca tgg gca att aaa aca tta ggt Ala Pro Leu Glu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu Gly 2085 2090 2095	6824
tta aaa ccc act tat tta ggt atg tta cgt gga tta gct taaggagcgt Leu Lys Pro Thr Tyr Leu Gly Met Leu Arg Gly Leu Ala 2100 2105 2110	6873

tga

6876

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 Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu
 35 40 45
 Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn
 50 55 60
 Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg
 65 70 75 80
 Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn
 85 90 95
 Leu Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala
 100 105 110
 Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser
 115 120 125
 Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys
 130 135 140
 Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala
 145 150 155 160
 Phe Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile
 165 170 175
 Thr Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser
 180 185 190
 Gly Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala
 195 200 205
 Leu Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu
 210 215 220
 Asn Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met
 225 230 235 240
 Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys
 245 250 255
 Ser Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro
 260 265 270
 Thr Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly
 275 280 285

Lys	Leu	Glu	Gly	Lys	Leu	Thr	Thr	Leu	Gln	Asn	Gly	Glu	Tyr	Ala	Glu	290	295	300
Arg	Gly	Lys	Phe	Asp	Glu	Ser	Ile	Gln	Ile	Gly	Lys	His	Gln	Leu	Ser	305	310	315
Leu	Pro	Ser	Val	Glu	Leu	Lys	Ala	Glu	Phe	Ser	Asp	Lys	Glu	Arg	Leu	325	330	335
Glu	Glu	Asp	Gly	Val	Asp	Leu	Ser	Ser	Ile	Ala	Glu	Leu	Leu	Glu	Met	340	345	350
Pro	Asn	Leu	Phe	Ile	Asp	Asn	Ser	Ile	Gln	Leu	Glu	Lys	Lys	Lys	Leu	355	360	365
Ser	Pro	Ile	Glu	Asp	Leu	Asp	Glu	Glu	Pro	Arg	Lys	Asn	Leu	Asp	Ile	370	375	380
Glu	Glu	Ser	His	Ser	Asn	Ser	Ser	Asp	Asp	Val	Leu	Ser	Met	Asn	Asp	385	390	395
Asp	Glu	Ser	Asp	Thr	Asp	Asp	Ser	Lys	Trp	Ser	Met	Gly	Asn	Asp	Glu	405	410	415
Lys	Glu	Met	Pro	Asp	Asp	Lys	Leu	Gly	Ile	Ser	Arg	Asp	Asp	Arg	Gly	420	425	430
Asn	Lys	Pro	Pro	Arg	Thr	Asp	Pro	Thr	Val	Asp	Tyr	Leu	Asn	Pro	Asp	435	440	445
Glu	Phe	Phe	Glu	Asn	Gly	Tyr	Leu	Leu	Asn	Glu	Leu	Leu	Gln	Glu	Leu	450	455	460
Gly	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Gly	Glu	Asp	His	Phe	Lys	Arg	Ser	465	470	475
Thr	Asn	Leu	Val	Arg	Leu	Gly	Glu	Arg	Asp	Arg	Gln	Asn	Arg	Glu	Lys	485	490	495
Arg	Glu	Lys	Glu	Gly	Tyr	Phe	Asp	Leu	Pro	Gly	Thr	Leu	Asp	Met	Lys	500	505	510
Leu	Gln	Glu	Leu	Phe	Glu	Lys	Arg	Lys	Gln	Lys	His	Glu	Ala	Glu	Gln	515	520	525
Lys	Ala	Arg	Ile	Glu	Lys	Ala	Leu	Leu	Gln	Lys	Ser	Glu	Gln	Gln	Glu	530	535	540
Lys	Arg	Val	Glu	Glu	Arg	Lys	Gln	Glu	Glu	Lys	Arg	Gln	Ala	Gln	Asp	545	550	555
Lys	Ile	Ala	Lys	Gln	Val	Glu	Ile	Ala	Lys	Glu	Met	Gln	Arg	Val	Glu	565	570	575
Glu	Ile	Arg	Gln	Arg	Glu	Lys	Gln	Leu	Ala	Ile	Gln	Leu	Gln	Glu	Glu	580	585	590
Glu	Lys	Lys	Gln	Gln	Glu	Glu	Lys	His	Leu	Ser	Glu	Glu	Lys	Lys	Gln	595	600	605
Ala	Glu	Gln	Lys	Gln	Lys	Ala	Glu	Glu	Lys	Val	Ala	Gln	Glu	Arg	Leu	610	615	620

Asp	Ile	Glu	Gln	Gln	Lys	Ala	Tyr	Glu	Glu	Met	Ala	Lys	Arg	Glu	Ala	625	630	635	640
Glu	Ala	Ser	Lys	Asn	Val	Leu	Leu	Lys	Ala	Ile	Asp	Glu	Glu	Arg	Pro	645	650	655	
Lys	Val	Glu	Thr	Asp	Pro	Leu	Phe	Arg	Thr	Lys	Leu	Lys	Tyr	Ile	Asn	660	665	670	
Gln	Asp	Asp	Tyr	Ala	Gly	Ala	Asn	Tyr	Phe	Phe	Asn	Lys	Val	Gly	Leu	675	680	685	
Asn	Thr	Lys	Gly	His	Gln	Lys	Val	Asn	Val	Leu	Gly	Asp	Asn	Tyr	Phe	690	695	700	
Asp	His	Gln	Val	Ile	Thr	Arg	Ser	Ile	Glu	Lys	Lys	Val	Asp	Asn	His	705	710	715	720
Leu	Asn	Gln	Lys	Tyr	Asn	Leu	Ser	Asp	Val	Glu	Leu	Val	Lys	Gln	Leu	725	730	735	
Met	Asp	Asn	Ser	Thr	Thr	Gln	Ala	Gln	Glu	Leu	Asp	Leu	Lys	Leu	Gly	740	745	750	
Ala	Ala	Leu	Thr	Lys	Glu	Gln	Gln	Ala	Asn	Leu	Thr	Gln	Asp	Ile	Val	755	760	765	
Trp	Tyr	Val	Lys	Thr	Lys	Val	Lys	Gly	Lys	Asp	Val	Phe	Val	Pro	Lys	770	775	780	
Val	Tyr	Phe	Ala	Ser	Glu	Thr	Leu	Val	Glu	Ala	Gln	Lys	Leu	Gln	Gly	785	790	795	800
Leu	Gly	Thr	Gly	Thr	Ile	Arg	Val	Gly	Glu	Ala	Lys	Ile	Lys	Ala	Lys	805	810	815	
Asp	Val	Val	Asn	Thr	Gly	Thr	Leu	Ala	Gly	Arg	Lys	Leu	Asn	Val	Glu	820	825	830	
Ala	Ser	Asn	Lys	Ile	Lys	Asn	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Gln	Glu	835	840	845	
Thr	Arg	Leu	Val	Gly	Arg	Lys	Gly	Ile	Glu	Asn	Val	Ser	Arg	Ser	Phe	850	855	860	
Ala	Asn	Asp	Glu	Leu	Gly	Val	Thr	Ala	Gln	Arg	Ser	Glu	Ile	Lys	Thr	865	870	875	880
Glu	Gly	His	Leu	His	Leu	Glu	Thr	Asp	Lys	Asp	Ser	Thr	Ile	Asp	Val	885	890	895	
Gln	Ala	Ser	Asp	Ile	Lys	Ala	Lys	Thr	Ser	Phe	Val	Lys	Thr	Gly	Asp	900	905	910	
Val	Asn	Leu	Lys	Asn	Thr	Tyr	Asn	Thr	Lys	His	Ala	Tyr	Arg	Glu	Lys	915	920	925	
Phe	Ser	Pro	Ser	Ala	Leu	Gln	Val	Ala	Glu	Leu	Asp	Val	Ala	Gly	Leu	930	935	940	
Lys	Val	Pro	Leu	Leu	Gly	Val	Ser	Ser	Pro	Ser	Ser	Tyr	Ser	Glu	His	945	950	955	960

Thr	Ser	Glu	Ala	Thr	Ser	Glu	Gly	Ser	Ile	Phe	Glu	Val	Gly	His	Leu	965	970	975	
His	Leu	Ala	Val	Asp	Arg	Asp	Val	Asn	Gln	Ala	Gly	Ser	Lys	Ile	Lys	980	985	990	
Ala	Lys	Tyr	Thr	Thr	Gly	Val	Val	Lys	Gly	Asn	Phe	Asn	Thr	Glu	Ala	995	1000	1005	
Gly	Lys	Asn	Ile	Lys	His	Val	Glu	Lys	Glu	Glu	Tyr	Ser	Ser	Gln	Leu	1010	1015	1020	
Phe	Ala	Ser	Ala	His	Ala	Ser	Gly	Gly	Gly	Thr	Ser	Val	Arg	Tyr	Asp	025	1030	1035	1040
Tyr	Asn	Ser	Gln	Asp	Gly	Gly	Asn	Ala	Ser	Val	Gly	Val	Pro	Thr	Asn	1045	1050	1055	
His	Thr	Gly	Val	Gly	Ala	Glu	Ala	Gly	Met	Ser	Phe	Thr	His	Thr	Lys	1060	1065	1070	
Asp	Lys	Glu	Thr	Leu	Leu	Thr	His	Thr	Asn	Ser	Glu	Leu	Gln	Val	Lys	1075	1080	1085	
His	Gly	Lys	Leu	His	Val	Leu	Gly	Tyr	Ala	Asp	Ile	Gly	Gly	Val	Asp	1090	1095	1100	
Ile	Asn	Thr	Lys	Leu	Pro	Glu	Asp	Ala	Gln	Ser	Lys	Ala	Gln	Lys	Glu	1105	1110	1115	1120
Ile	Ala	Ala	Ser	Lys	Pro	Glu	Lys	Thr	Glu	Gln	Ser	Ala	Gln	Asp	Val	1125	1130	1135	
Ala	Gln	Ala	Gln	Ser	Asn	Ala	Asn	Lys	Asp	Lys	Glu	Asn	Lys	Ala	Pro	1140	1145	1150	
Glu	Ile	Lys	Glu	Leu	Ser	Glu	Ala	Glu	Ile	Ala	Asp	Leu	Met	Ser	Glu	1155	1160	1165	
Lys	Ser	Lys	Ala	Tyr	Phe	Asp	Asp	Phe	Ala	Glu	Gln	Ala	Lys	Lys	Ala	1170	1175	1180	
Pro	Glu	Asn	Asn	Arg	Phe	Glu	Leu	Ser	Ala	Lys	Glu	Ile	Lys	Ser	Ser	1185	1190	1195	1200
Lys	Gln	Lys	Asp	Gln	Tyr	Asp	His	Glu	Ser	Glu	Arg	Thr	Thr	Phe	Lys	1205	1210	1215	
Val	Gly	Pro	Glu	Ala	Glu	Ala	His	Ser	Ala	Val	Ala	Asp	Met	Val	Ser	1220	1225	1230	
His	Leu	Val	Lys	Glu	Tyr	Arg	Asp	Ala	Gln	Asn	Gly	Thr	Lys	Gln	Asp	1235	1240	1245	
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Gly	Asp	Leu	Ala	Gly	Ser	Ser	Ala	Lys	Leu	Ser	Val	Glu	Arg	Thr	His	265	1270	1275	1280
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Lys	Thr	Leu	Phe	Ser	Val	Pro	Ile	Val	Asp	Ala	Lys	Val	Lys	Met	Leu	905	1910	1915 1920
Phe	Ala	Glu	Lys	Asn	Ile	Gln	Val	Asn	Tyr	Asp	Arg	Ser	Leu	Thr	Ala	1925	1930	1935
Ile	Asp	Leu	Ser	Lys	Arg	Ile	Ala	Thr	Phe	Asn	Ser	Pro	Glu	Gly	Val	1940	1945	1950
Val	Glu	Val	Pro	Tyr	Asp	Phe	Ile	Asn	Val	Val	Pro	Pro	Met	Arg	Ala	1955	1960	1965

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His Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn
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Lys Leu Ile Phe Ser Gln Val Lys Gly Cys Leu Val Pro Val Ala Glu
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Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser Ser Asp Ser Thr Ser Thr
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tcc tcc gtg tct tta tta gta aaa agc acg ttc aat cct gtt tcg tat 1688
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gca atg caa ttg act tgg aaa cag ctt tct att tta ttt tta act gtg 1736
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Ile Ser Val Pro Val Leu Ala Glu Gly Lys Gly Asp Glu Arg Asn Gln
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Leu Thr Val Ile Asp Asn Ser Asp His Ile Lys Leu Asp Ala Ser Asn
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ctt gct ggt aat gat aaa aca aaa atc tat caa gca gaa aat aaa gtt 1880
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Gly Lys Lys Ala Asp Ile Val Ile Ala Asn Gln Asn Gly Ile Thr Leu	
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Val Ile Ile Asp Ile Asp Gly Phe Ser Thr Asp Gly Leu Lys Tyr Leu	
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Glu Tyr Asp Leu Ser Lys His Glu Leu Lys Lys Thr Ser Gly Glu Asn	
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His Gly Lys Asn Ile Lys Leu Ile Val Thr Asp Lys Gly Ala Gly Val	
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Lys His Asp Gly Ile Ile Leu Ser Glu Asn Asp Ile Gln Ile Glu Met	
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Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr Ile Gln Gln Thr Val Val	
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Ala	Asn	Arg	Val	Phe	Val	Gly	Ser	Gln	Thr	Lys	Ser	Asp	Glu	Ile	Ser	
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Phe	Ser	Ile	Ser	Pro	Ser	Met	Leu	Ala	Ser	Leu	Ser	Ala	Gln	Phe	Lys	
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370 375 380

Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
385 390 395 400

Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
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Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
420 425 430

Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
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Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
450 455 460

Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
465 470 475 480

Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
485 490 495

Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
500 505 510

Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
515 520 525

Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
530 535 540

Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
545 550 555 560

Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
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<213> Pasteurella multocida

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<222> (1)..(1446)

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His	Ala	Tyr	Gln	Asn	Gln	Pro	Leu	Ser	Thr	Lys	Val	Val	Phe	Gln	Leu	
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gtg	aaa	gat	ttg	acg	gaa	ggt	tta	tac	cgt	tct	ggc	tac	gtg	aca	agt	144
Val	Lys	Asp	Leu	Thr	Glu	Val	Leu	Tyr	Arg	Ser	Gly	Tyr	Val	Thr	Ser	
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Ala	Ile	Gly	Leu	Lys	Asn	Ser	Lys	Ile	Ser	Asn	Gly	Asp	Leu	Glu	Phe	
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Pro	Thr	Arg	Phe	Arg	Asp	Lys	Thr	Met	Leu	Ser	Val	Leu	Pro	Asn	Leu	
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atc	gga	aat	cgc	tta	agt	att	cac	gac	att	gac	cag	ttg	atc	gaa	atc	336
Ile	Gly	Asn	Arg	Leu	Ser	Ile	His	Asp	Ile	Asp	Gln	Leu	Ile	Glu	Ile	
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Leu	Asn	Thr	Thr	Asn	Lys	Lys	Ala	Thr	Val	Asn	Val	Val	Ala	Ser	Glu	
		115					120					125				
gaa	aaa	ggc	agc	tca	aat	cta	aat	att	gaa	aga	caa	tat	gat	ggt	ttt	432
Glu	Lys	Gly	Ser	Ser	Asn	Leu	Asn	Ile	Glu	Arg	Gln	Tyr	Asp	Val	Phe	
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Pro	Gln	Val	Ser	Val	Gly	Phe	Asn	Asn	Ser	Gly	Ala	Gly	Asn	Asn	Ala	
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Asn	Gly	Arg	Asn	Gln	Ala	Thr	Leu	Asn	Ile	Ala	Trp	Ser	Asp	Leu	Leu	
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ggc	acg	aat	gat	cgt	tgg	agt	ttc	tcg	agt	agt	tac	cgt	tta	tat	aaa	576
Gly	Thr	Asn	Asp	Arg	Trp	Ser	Phe	Ser	Ser	Ser	Tyr	Arg	Leu	Tyr	Lys	
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Asn	His	His	Ala	Asn	Gln	Gln	Arg	Asn	Tyr	Thr	Leu	Ser	Tyr	Ser	Gln	
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Pro	Ile	Gly	Phe	Ser	Thr	Val	Glu	Ile	Lys	Ala	Ser	Glu	Ser	Thr	Tyr	
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Glu	Lys	Glu	Leu	Arg	Gly	Ile	Asn	Thr	His	Ser	Ser	His	Gly	Lys	Thr	
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caa	agc	tta	gct	gtc	aag	ctg	atg	cat	gtg	tta	ttg	cgt	aat	aag	gag	768
Gln	Ser	Leu	Ala	Val	Lys	Leu	Met	His	Val	Leu	Leu	Arg	Asn	Lys	Glu	
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agt	att	tta	tct	aca	tat	acc	gag	ttc	gag	ttt	aaa	aaa	cgg	att	agt	816
Ser	Ile	Leu	Ser	Thr	Tyr	Thr	Glu	Phe	Glu	Phe	Lys	Lys	Arg	Ile	Ser	
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tat ttt tct gat att ttg att ggg aaa tat cac aat aat aaa gtg agc	864
Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser	
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gta ggg tta tct tac atg act aat ttt gct tac ggg aag ctt tac agc	912
Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser	
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Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser	
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Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser	
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Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr	
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Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu	
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Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly	
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385 390 395 400	
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Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe	
405 410 415	
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Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr	
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acc act tta gtc ggt ttt gcc cta ggc ttg aaa acg caa ata aag tta	1344
Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu	
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Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly	
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Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu	
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Ser Phe	
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<213> Pasteurella multocida

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Val	Lys	Asp	Leu	Thr	Glu	Val	Leu	Tyr	Arg	Ser	Gly	Tyr	Val	Thr	Ser	
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Pro	Thr	Arg	Phe	Arg	Asp	Lys	Thr	Met	Leu	Ser	Val	Leu	Pro	Asn	Leu	
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Ile	Gly	Asn	Arg	Leu	Ser	Ile	His	Asp	Ile	Asp	Gln	Leu	Ile	Glu	Ile	
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Leu	Asn	Thr	Thr	Asn	Lys	Lys	Ala	Thr	Val	Asn	Val	Val	Ala	Ser	Glu	
		115					120					125				
Glu	Lys	Gly	Ser	Ser	Asn	Leu	Asn	Ile	Glu	Arg	Gln	Tyr	Asp	Val	Phe	
	130					135					140					
Pro	Gln	Val	Ser	Val	Gly	Phe	Asn	Asn	Ser	Gly	Ala	Gly	Asn	Asn	Ala	
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			180					185					190			
Asn	His	His	Ala	Asn	Gln	Gln	Arg	Asn	Tyr	Thr	Leu	Ser	Tyr	Ser	Gln	
		195					200					205				
Pro	Ile	Gly	Phe	Ser	Thr	Val	Glu	Ile	Lys	Ala	Ser	Glu	Ser	Thr	Tyr	
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Glu	Lys	Glu	Leu	Arg	Gly	Ile	Asn	Thr	His	Ser	Ser	His	Gly	Lys	Thr	
225					230					235					240	
Gln	Ser	Leu	Ala	Val	Lys	Leu	Met	His	Val	Leu	Leu	Arg	Asn	Lys	Glu	
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Ser	Ile	Leu	Ser	Thr	Tyr	Thr	Glu	Phe	Glu	Phe	Lys	Lys	Arg	Ile	Ser	
			260					265					270			
Tyr	Phe	Ser	Asp	Ile	Leu	Ile	Gly	Lys	Tyr	His	Asn	Asn	Lys	Val	Ser	
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Val	Gly	Leu	Ser	Tyr	Met	Thr	Asn	Phe	Ala	Tyr	Gly	Lys	Leu	Tyr	Ser	
	290					295					300					
Asp	Ile	Ala	Tyr	Ala	Asn	Gly	Leu	Arg	Trp	Phe	Gly	Ala	Asn	Tyr	Ser	
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Ala	Tyr	Asp	Ala	Asn	Arg	Glu	Lys	Thr	Leu	Lys	Leu	Leu	Ser	Gly	Ser	
				325					330					335		
Ile	Asn	Trp	Gln	Arg	Pro	Ile	Ser	Leu	Phe	Glu	Arg	Ala	Met	Asn	Tyr	
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Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu
355 360 365

Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly
370 375 380

Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr
385 390 395 400

Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
405 410 415

Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
420 425 430

Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
435 440 445

Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly
450 455 460

Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
465 470 475 480

Ser Phe

<210> 21
<211> 1170
<212> DNA
<213> Pasteurella multocida

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<222> (639)..(1022)

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<223> greA

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tttcaaattg aaattgggtca cttagtagca gtttggcggg taaggcgggt agcacttttt 240
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ttaagttttt agccacaaaa ctaggctggg tcccttcggg taaatgagcg ttgatttcag 360
caagatcaat ctacgcataa ctgaaatgac tgacgagtaa actacatata agtatcgttc 420
gtttgaaaag gcgtaaaagc gtggcagtaa aaaaagaaga tattttatac ataattgggt 480
cgagcagttg ctattttttt attgtcgaac aataatagta tttgaaccct cgagagtaaa 540
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Ile Ala Glu Ala Arg Glu His Gly Asp Leu Lys Glu Asn Ala Glu Tyr
35 40 45
His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu
50 55 60
Ile Glu Gly Lys Leu Ala Asn Ser Gln Ile Ile Asp Val Thr Lys Ile
65 70 75 80

Pro	Asn	Asn	Gly	Lys	Val	Ile	Phe	Gly	Ala	Thr	Ile	Leu	Leu	Leu	Asn
				85					90					95	
Ile	Asp	Thr	Glu	Glu	Glu	Val	Ser	Tyr	Gln	Ile	Val	Gly	Asp	Asp	Glu
			100					105					110		
Ala	Asn	Ile	Lys	Ala	Gly	Leu	Ile	Ser	Val	Asn	Ala	Thr	Arg	Leu	Asn
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gcgatcaatt tattccgac aatcggttggt aatacttcaa tcagctctgc ccaagggtga	180
tcaatttgct gtgtttgttt tgggaaaagac aaattaatgc caaagccaat cacgagatta	240
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aatagcacat catttgGCCA tttaaatcca atgttcaaag cacctgcttg ctttagcggt	360
tctgCGATTG ccatacccac tactaaactc aagccttcta aattgacctt ttggTcacaT	420
gCCCAATACA aactcataat cacttgTCCA gcaaaaggag aaagccattg acgaccacgt	480
cgtccacgtc cgcCAGTTTG atattctgct aagCAAAtAg cgCCTTTTTc caaatgtgCa	540
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agcaacgAAA tctgtataat gcgaccgcaa tatttttttac ctttttattt ttcatatcaa	960
cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc	1012
Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe	
1 5 10	
gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc	1060
Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr	
15 20 25	

gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca	1108
Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro	
30 35 40	
atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc	1156
Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile	
45 50 55	
tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct	1204
Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser	
60 65 70 75	
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Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser	
80 85 90	
ggg att gta tcc gat cct gtc acc gtt tca cca acc tta tct tta gca	1300
Gly Ile Val Ser Asp Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala	
95 100 105	
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Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val	
110 115 120	
gtt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca	1396
Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr	
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Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile	
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Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser	
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Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys	
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Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly	
270 275 280	

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Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile	
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Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val	
300 305 310 315	
cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg	1972
Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg	
320 325 330	
ggt att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att	2020
Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile	
335 340 345	
tcg aaa gcc att gcg gcg ggc gcc tct tgt gtt atg gtg ggt tcc atg	2068
Ser Lys Ala Ile Ala Ala Gly Ala Ser Cys Val Met Val Gly Ser Met	
350 355 360	
ttt gca ggt aca gaa gaa gca cca ggt gaa atc gaa ctt tat caa ggt	2116
Phe Ala Gly Thr Glu Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly	
365 370 375	
cgt gcc ttt aaa tct tat cga ggt atg gga tcg tta ggt gcg atg agc	2164
Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser	
380 385 390 395	
aaa ggc tca agc gac cgc tat ttc cag tcc gat aat gca gct gac aaa	2212
Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys	
400 405 410	
tta gta cca gaa ggt att gaa gga cgt att cca tat aaa gga ttc tta	2260
Leu Val Pro Glu Gly Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu	
415 420 425	
aaa gaa att atc cat caa caa atg ggt gga ttg cgt tct tgt atg ggc	2308
Lys Glu Ile Ile His Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly	
430 435 440	
tta acg ggt. tgt gca acc att gat gaa ctc cgt acc aaa gcg cag ttt	2356
Leu Thr Gly Cys Ala Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe	
445 450 455	
gtg cgc att agt ggt gca ggg atc caa gaa agc cat gtg cat gat gtg	2404
Val Arg Ile Ser Gly Ala Gly Ile Gln Glu Ser His Val His Asp Val	
460 465 470 475	
act atc aca aaa gaa gcc cct aat tat cgt atg ggt taaacattgc	2450
Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly	
480 485	
ttaggtgggg attatcccca cctaagttta ttttaaataa caacgttaat agagaagctt	2510
atttttatgt atggcattaa aattaaaaat gttattaaac tttttctatt aaagttttta	2570
agaaataaat atcgaataa aatcaatatt caacatcatc tcattagtat tgaaggaaaa	2630
tgcggtgagt ttgatttaag ccagctaaac tatgttttatt tggtgaaaga tcctgagata	2690
agaaataatc gactgacact gtacttgaat gatttttttca aaattggggg aaattatcat	2750
ggatttactc aaatgtatca gacactatca tccaagtatg gttttgatga cgcaacgttt	2810

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caaaattatg tgattcttga tgaagcctat actgactata cacaagggtt tgaaattcaa 2930
tctcctgaaa aaatatattat tccttggggg actacttatg aagccttatt tcagcagaca 2990
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tataagtctg ttttacgcct taacgcgaca gaatttgaat tgcgttatta tcgacatata 3290
cgagacgatt ttgatagggg atacactaaa ttcagcatta gagatacgac agactattta 3350
gattatgtga tcaacgagcc ttatgaaaat caattagtga taacggatta tttagtгatt 3410
gaggcgcaaa atttaataaa aatggattat accgataatt ccattattaa acgccgacca 3470
ccaaaaataa aagaaaagtt tcgtgatgca caaagcctga tttggacaga tgatctcaat 3530
cataaaatcg gttttaccag tgatgaccgc gctatcgtct ttgataaagc ggacattgaa 3590
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tgttttgtgg ataaaaataa ggaagccatc actgtatttc tagctgaaca tcattttctg 3710
ataccctatg tggataaaat aaaaacactg acacaaaaag aggtgttggt tcttgaagaa 3770
tatatagagg atgtttaaaa aaccgataac atcttgatgt catcgcaaат tcaaaactct 3830
tttacacaat atattttaac tttaaccgga tttaatatтt acgtaaaaac aactaagaga 3890
acttaaатga acaacattca caaccataaa attttaattt tggacttcgg ttcacaatat 3950
accagttga ttgcccgccg tgtacgtgaa attggcgtgt actgcgaact ttgggcatgg 4010
gatgtatccg aagccgatat tcgtgagttt aatccaactg ggattattct ttctgggtgg 4070
cctgaaagta cactgaaga aaacagccca cgagctcccg aatacgtatt caacgccggт 4130
gtacccgтat tagggatctg ttatggtatg caaaccatgg cgatgcaact aggtgggtta 4190
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tcaacctgtc caatcgcagc tatgtcggat gaacgtcgtc gtttttatgg tgtccaattc 4430
caccagaag tgactcatac aaaaagcggg cttgaattat taacgaattt tgtggтgaag 4490
atctgtgggt gtgaacgtaa ctggacacca gaaaatatca ttgaagatgc cgttgctcgt 4550
cttaaagcac aagtgggcga tgatgaagtg attttaggct tatctggтgg cgttaactgc 4610
cgtataggca gcttagaaaa agtgtccgcg ctcacgttaa tccccgtaag cgттga 4666

<210> 24
 <211> 487
 <212> PRT
 <213> Pasteurella multocida

<400> 24
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 1 5 10 15
 Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
 20 25 30
 Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
 35 40 45
 Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
 50 55 60
 Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
 65 70 75 80
 Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Asp
 85 90 95
 Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu
 100 105 110
 Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys
 115 120 125
 Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
 130 135 140
 Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val
 145 150 155 160
 Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His
 165 170 175
 Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu
 180 185 190
 Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro
 195 200 205
 Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
 210 215 220
 Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
 225 230 235 240
 Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
 245 250 255
 Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
 260 265 270
 Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
 275 280 285
 Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
 290 295 300

Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
 305 310 315 320
 Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile
 325 330 335
 Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile Ser Lys Ala Ile Ala
 340 345 350
 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu
 355 360 365
 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
 370 375 380
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
 385 390 395 400
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
 405 410 415
 Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His
 420 425 430
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
 435 440 445
 Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly
 450 455 460
 Ala Gly Ile Gln Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu
 465 470 475 480
 Ala Pro Asn Tyr Arg Met Gly
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<210> 25
 <211> 2364
 <212> DNA
 <213> Pasteurella multocida

<220>
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 <222> (191)..(1828)

<220>
 <223> Hi1501

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 aattgacggc gatttagggc gtgatgaatt tgatgacggc gatttataca gtatttggcg 180
 gagataaaaa atg gcg aag aaa aag aaa aaa tta caa caa gcg aaa aaa 229
 Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys
 1 5 10
 gta caa gtt ggc tta gat aca caa aca aat gag gcg cgt gtc acg gag 277
 Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu
 15 20 25

aca gga aga att att tct gat cac cca agc aat aaa att acc ccc gca	325
Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala	
30 35 40 45	
aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg	373
Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala	
50 55 60	
caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg	421
Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly	
65 70 75	
gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc	469
Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg	
80 85 90	
att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc	517
Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val	
95 100 105	
gaa att gac gag ctt ttc tat caa ttc cca atg cta gaa gat tta atg	565
Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met	
110 115 120 125	
gtg gat atg atg gat gcg gta gga cat ggt ttt tcg gcg tta gaa att	613
Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile	
130 135 140	
gaa tgg aag caa gct gaa agt aaa tgg att cca gtt aat ttt atc gca	661
Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala	
145 150 155	
cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt	709
Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu	
160 165 170	
aaa acg cca gat aat caa gac ggt gag ccg ttg aga caa tat ggc tgg	757
Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp	
175 180 185	
gta gtg cat acc cac aaa tca aga aca gta cag ctt gct cgt atg ggt	805
Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly	
190 195 200 205	
tta ttt aga acg ctc gca tgg ctt tat atg ttt aaa cac tac tcg gtg	853
Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val	
210 215 220	
cat gat ttt gcc gaa ttt cta gag ctt tat ggt atg ccg att cgt att	901
His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile	
225 230 235	
ggt aaa tac cca ttt ggg gca acg aat gac gaa aag cgc aca tta ttg	949
Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu	
240 245 250	
cgt gca ctt gct caa atc gga cat aac gca gca ggg att atg cca gaa	997
Arg Ala Leu Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu	
255 260 265	
gga atg aat gtt gag ttg cat aat gtg aca aac act act ggc tcg gct	1045
Gly Met Asn Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala	
270 275 280 285	

gga agc aac ccg ttt ttg caa atg gtg gac tgg tgt gaa aag tcc gcc	1093
Gly Ser Asn Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala	
290 295 300	
gca cgt ttg att cta ggg caa aca tta aca agc ggt gca gat ggt aaa	1141
Ala Arg Leu Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys	
305 310 315	
act tca act aat gcc ctt gga caa gtg cat aat gaa gtc aga cgt gac	1189
Thr Ser Thr Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp	
320 325 330	
ttg ctt gtg tct gat gct aaa cag att gca caa act att aca caa cag	1237
Leu Leu Val Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln	
335 340 345	
att att ctg cca tat ctt caa att aac att gat ccg aat att ttg cct	1285
Ile Ile Leu Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro	
350 355 360 365	
tct cgt gtg ccg tat ttc gag ttt gac acg aaa gaa tat gct gat tta	1333
Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu	
370 375 380	
agt gtc cta gcg gat gct att cct aag ctt gtg agc gta gga gtg cgc	1381
Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg	
385 390 395	
att cct gaa aat tgg gtg cgt gat aaa gcg ggc att cca gaa ccg cag	1429
Ile Pro Glu Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln	
400 405 410	
gaa aat gaa acg att tta agt gcg gtt caa cat gat ttt aaa aca gat	1477
Glu Asn Glu Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp	
415 420 425	
tta aac gat gtt gaa aat ccg aaa aaa cag acc gca ctt tct gta caa	1525
Leu Asn Asp Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln	
430 435 440 445	
aat cac gtg aca ggt tgt cag tgt gat ggc tgt cgt ggt gtt gca tta	1573
Asn His Val Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu	
450 455 460	
tct gcg aat aat aac agt tct act gcg cag ggc gtg cta gat ggt gga	1621
Ser Ala Asn Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly	
465 470 475	
ctt gcg caa gca ttt aat gag cct gat ttt aat aaa caa tta aat cca	1669
Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro	
480 485 490	
atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat	1717
Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp	
495 500 505	
gag gcg gca gaa aaa ctc gct gaa gca tac cca gaa att tca agt cac	1765
Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His	
510 515 520 525	
gaa cac gaa cag tat ctc tca aat gcg ctg ttt tta gct gat tta ctt	1813
Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu	
530 535 540	

gga gga act aat gtc taaaccgctt agttttctat tcggacttga accaacgcaa 1868
Gly Gly Thr Asn Val
545

gccattgagt ttttacataa taaaaaatta cttgcaacga aagtgtttaa aaaatcactg 1928
catgatagtg ccatcgcaag agctacaaca atcgcgagat tatctagtct tgagatgacg 1988
aatgatattt ataaatcaat ggaagttgcc aaaaaagagg gtaagagctt tacacaatgg 2048
aaaaaagact tggtaagtga gtttgagaaa aaaggctggg tattcgggca tgataaatct 2108
atcagtcgcg gtatcgacgg aaaactgttg gctgatccga aaacaggcga atattttggt 2168
acaccgcgtc ggctgaatac aatttatcgt acaaacgtgc aagccgcata ttctgcggcg 2228
cgctatcagc gcatgatgga taatattgat catcgcccct attggcaata ttccgctgtc 2288
agcgatgagc gtacacgacc ctctcatctt gcactaaacg gtcgaattta tcgctatgat 2348
gacccgtttt ggtcga 2364

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<211> 546
<212> PRT
<213> Pasteurella multocida

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Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu Thr Gly Arg
20 25 30
Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala Lys Leu Lys
35 40 45
Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala Gln His Glu
50 55 60
Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly Ala Asn Ile
65 70 75 80
Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg Ile Ala Glu
85 90 95
Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val Glu Ile Asp
100 105 110
Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met Val Asp Met
115 120 125
Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile Glu Trp Lys
130 135 140
Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala Arg Pro Gln
145 150 155 160
Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu Lys Thr Pro
165 170 175
Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp Val Val His

180						185						190					
Thr	His	Lys	Ser	Arg	Thr	Val	Gln	Leu	Ala	Arg	Met	Gly	Leu	Phe	Arg		
		195					200					205					
Thr	Leu	Ala	Trp	Leu	Tyr	Met	Phe	Lys	His	Tyr	Ser	Val	His	Asp	Phe		
	210					215					220						
Ala	Glu	Phe	Leu	Glu	Leu	Tyr	Gly	Met	Pro	Ile	Arg	Ile	Gly	Lys	Tyr		
225					230					235					240		
Pro	Phe	Gly	Ala	Thr	Asn	Asp	Glu	Lys	Arg	Thr	Leu	Leu	Arg	Ala	Leu		
				245					250					255			
Ala	Gln	Ile	Gly	His	Asn	Ala	Ala	Gly	Ile	Met	Pro	Glu	Gly	Met	Asn		
			260					265					270				
Val	Glu	Leu	His	Asn	Val	Thr	Asn	Thr	Thr	Gly	Ser	Ala	Gly	Ser	Asn		
		275					280					285					
Pro	Phe	Leu	Gln	Met	Val	Asp	Trp	Cys	Glu	Lys	Ser	Ala	Ala	Arg	Leu		
	290					295					300						
Ile	Leu	Gly	Gln	Thr	Leu	Thr	Ser	Gly	Ala	Asp	Gly	Lys	Thr	Ser	Thr		
305					310					315					320		
Asn	Ala	Leu	Gly	Gln	Val	His	Asn	Glu	Val	Arg	Arg	Asp	Leu	Leu	Val		
				325					330					335			
Ser	Asp	Ala	Lys	Gln	Ile	Ala	Gln	Thr	Ile	Thr	Gln	Gln	Ile	Ile	Leu		
			340					345					350				
Pro	Tyr	Leu	Gln	Ile	Asn	Ile	Asp	Pro	Asn	Ile	Leu	Pro	Ser	Arg	Val		
		355					360					365					
Pro	Tyr	Phe	Glu	Phe	Asp	Thr	Lys	Glu	Tyr	Ala	Asp	Leu	Ser	Val	Leu		
	370					375					380						
Ala	Asp	Ala	Ile	Pro	Lys	Leu	Val	Ser	Val	Gly	Val	Arg	Ile	Pro	Glu		
385					390					395					400		
Asn	Trp	Val	Arg	Asp	Lys	Ala	Gly	Ile	Pro	Glu	Pro	Gln	Glu	Asn	Glu		
				405					410					415			
Thr	Ile	Leu	Ser	Ala	Val	Gln	His	Asp	Phe	Lys	Thr	Asp	Leu	Asn	Asp		
			420					425					430				
Val	Glu	Asn	Pro	Lys	Lys	Gln	Thr	Ala	Leu	Ser	Val	Gln	Asn	His	Val		
		435					440						445				
Thr	Gly	Cys	Gln	Cys	Asp	Gly	Cys	Arg	Gly	Val	Ala	Leu	Ser	Ala	Asn		
	450					455					460						
Asn	Asn	Ser	Ser	Thr	Ala	Gln	Gly	Val	Leu	Asp	Gly	Gly	Leu	Ala	Gln		
465					470					475					480		
Ala	Phe	Asn	Glu	Pro	Asp	Phe	Asn	Lys	Gln	Leu	Asn	Pro	Met	Val	Lys		
				485					490					495			
Lys	Ala	Val	Ala	Val	Leu	Met	Ala	Cys	Asp	Ser	Tyr	Asp	Glu	Ala	Ala		
			500					505					510				
Glu	Lys	Leu	Ala	Glu	Ala	Tyr	Pro	Glu	Ile	Ser	Ser	His	Glu	His	Glu		

515	520	525
Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu Gly Gly Thr		
530	535	540
Asn Val		
545		
<210> 27		
<211> 1353		
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<222> (2)..(1351)		
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<223> Nucleotides at positions 375, 399, 423, and 453 are A, T, C or G. The corresponding amino acids are unknown.		
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Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu		
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ttt tta gaa gat cgc cgt gaa aag aag ctt acc gaa gaa aaa aca tta 97		
Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu		
20	25	30
ggg ctt agt gat gca gtg cgt ttt gct aat gat caa acc cct tat ctc 145		
Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu		
35	40	45
cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193		
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr		
50	55	60
gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241		
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu		
65	70	75 80
caa gag ttt gat att aat aat agg aat aaa ttg gat tcg act atg tcg 289		
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser		
85	90	95
ttt gta tat tta caa aga cag aat ata gct cgg gga gaa ttt tca acg 337		
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr		
100	105	110
agt cct tta tat tgg ggg ccg agt cgc cat cgt tta tnt gcg aaa ttc 385		
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe		
115	120	125
gaa ttt cgt gat ang ttt tta gaa aat atg aat aag cnt ttt acg ttt 433		
Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe		
130	135	140

cgg ccg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat	481
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr	
145 150 155 160	
aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg	529
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met	
165 170 175	
gac gac att aag att ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg	577
Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg	
180 185 190	
tgg gat cac tat aac tat aag cca tta tta aat tct cag cat aat atc	625
Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile	
195 200 205	
aac agg aca cag aga tta cct tat cca aaa aca tca tcc aaa ttt tcg	673
Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser	
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Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His	
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Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu	
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Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe	
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Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala	
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Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu	
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Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys	
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Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu	
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Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
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aaa gat gcg ata gaa acg gaa tac aca cat gat aaa aag gtt gtc aaa 1297
Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys
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caa tgg ccg cat tta agt cca tcc tac ttt gtt gtt gat ttt acg ggg 1345
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 <213> Pasteurella multocida

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Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser

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Met Asp Lys Asn Leu Met Lys Gly Cys Val Phe Leu Ser Ile Val Gly
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Cys Gly Ile Gln Ile Gly Leu Ala Ser Asn Pro Asn Pro Pro Asp Val
20 25 30

gat gag tta tta cct att att gtg aat gct gat gaa gat aat aaa tta 1221
Asp Glu Leu Leu Pro Ile Ile Val Asn Ala Asp Glu Asp Asn Lys Leu
35 40 45

cca ggt cgt tct gta tta aaa cag aaa aat atc gat caa caa caa gca 1269
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Pro	Trp	Ala	Ala	Lys	Arg	Asp	Val	Met	Ser	Arg	Pro	Thr	Glu	Thr	Glu		
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Ile	Lys	His	Tyr	Gly	Ile	Asp	Val	Ala	Trp	Lys	Arg	Lys	Leu	Val	Tyr		
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Gln Pro Tyr Tyr Met Pro Ser Gly Arg Gln Tyr Thr Gln Ala Phe Tyr	
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Tyr Asn Asp Ile Ser Ala Gly His Asp Tyr Ser Gln Lys Asn Tyr Asn	
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Gly Trp Ser Tyr Tyr Leu Gly Leu Lys Tyr Asp Val Asn His Tyr Leu	
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Pro	Gly	Arg	Ser	Val	Leu	Lys	Gln	Lys	Asn	Ile	Asp	Gln	Gln	Gln	Ala	50	55	60	
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Ile	Lys	His	Tyr	Gly	Ile	Asp	Val	Ala	Trp	Lys	Arg	Lys	Leu	Val	Tyr	275	280	285	
Arg	Asp	Gln	Lys	Asp	Glu	Ser	Tyr	Ser	Leu	Lys	Tyr	Arg	Tyr	Leu	Pro	290	295	300	
Glu	Asn	Asn	Lys	Trp	Ile	Asn	Leu	Ser	Val	Gln	Leu	Ser	Tyr	Ser	Lys	305	310	315	320

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Tyr Leu Thr Trp Glu Ser Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser	
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Asn Leu Ile Asn Gln Lys Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser	
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Pro Gly Arg Asn Phe Lys Leu Ser Ala Glu Ile Thr Phe	
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 Glu Lys Lys Ile Gly Glu Thr Val Lys Thr Ala Ser Gln Leu Lys Arg
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 Gln Gln Val Gln Asp Ser Arg Asp Leu Val Arg Tyr Glu Thr Gly Val
 65 70 75 80
 Thr Val Val Glu Ala Gly Arg Phe Gly Ser Ser Gly Tyr Ala Ile Arg
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 Gly Val Asp Glu Asn Arg Val Ala Ile Thr Val Asp Gly Leu His Gln
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 Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys Glu Leu Phe Glu Gly Tyr
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Glu	Lys	Ala	Asp	Pro	Tyr	Thr	Ile	Thr	Lys	Glu	Ser	Thr	Leu	Val	Lys	245	250	255
Phe	Ser	Phe	Ser	Pro	Thr	Glu	Asn	His	Arg	Phe	Thr	Val	Ala	Ser	Asp	260	265	270
Thr	Tyr	Leu	Gln	His	Ser	Arg	Gly	His	Asp	Leu	Ser	Tyr	Asn	Leu	Val	275	280	285
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Ile	Thr	Thr	Arg	Ala	Arg	Thr	Glu	Asp	Tyr	Cys	Asp	Gly	Asn	Glu	Leu	340	345	350
Cys	Asp	Ser	Tyr	Lys	Asn	Pro	Leu	Gly	Leu	Gln	Phe	Lys	Asp	Gly	Gln	355	360	365
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Gly	Phe	Trp	Leu	Asp	Cys	Ser	Val	Phe	Asp	Cys	Asn	Lys	Pro	Phe	Thr	420	425	430
Val	Tyr	Asn	Ile	Ser	Asn	Gly	Thr	Tyr	Gln	Ala	Arg	Glu	Val	Leu	Leu	435	440	445
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Glu	Gly	Gly	Leu	Pro	Asn	Tyr	Leu	Ile	Leu	Pro	Asn	Ser	Lys	Gly	Tyr	465	470	475
Leu	Pro	Tyr	Asp	Tyr	Lys	Glu	Arg	Asp	Leu	Asn	Thr	Asn	Thr	Lys	Gln	485	490	495
Ile	Asn	Leu	Asp	Leu	Thr	Lys	Thr	Phe	Leu	Thr	Phe	Asn	Ile	Glu	Asn	500	505	510

Asn	Leu	Ser	Tyr	Gly	Gly	Val	Tyr	Ser	Arg	Ile	Glu	Lys	Glu	Met	Ile
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Lys	His	Glu	Pro	Leu	Thr	Ser	Phe	Leu	Ile	Pro	Val	Glu	Ala	Thr	Thr
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Ser	Asn	Ser	Val	Gly	Gly	Gln	Ala	Gln	Ala	Arg	Asp	Phe	Gln	Val	Tyr
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Asp His Lys Glu Asn Lys Phe Gly Ala Asp Leu Tyr Ile Thr Arg Val
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Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln
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Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu
885 890 895

Val Asp Ala Val Gly Tyr Ile Lys Pro Ile Lys Asn Leu Thr Leu Gln
900 905 910

Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser
915 920 925

Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser Asn Leu Ile Asn Gln Lys
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Leu Ser Ala Glu Ile Thr Phe
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acc Thr	ata Ile	caa Gln	gaa Glu	aga Arg	cga Arg	ggt Gly	tat Tyr	tgt Cys	ttt Phe	gac Asp	aaa Lys	cgt Arg	gca Ala	tat Tyr	att Ile	1228
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cat His	gag Glu	ctt Leu	tat Tyr	act Thr	gag Glu	caa Gln	gag Glu	tta Leu	att Ile	gat Asp	cgg Arg	ggg Gly	att Ile	gaa Glu	tat Tyr	1276
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Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln
35 40 45
Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser
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Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr
65 70 75 80
Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr
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Thr Phe Ile Asp Glu Gly Gly Asp Gly Tyr Pro Asp Asp Asp Gly Tyr
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Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys

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Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
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30              35              40

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Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu
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Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val
60              65              70

caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca 591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala
75              80              85

gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat 639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp

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Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val				
190 195 200				
tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga	975			
Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg				
205 210 215				
ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa	1023			
Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu				
220 225 230				
aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa	1071			
Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys				
235 240 245				
gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa	1119			
Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys				
250 255 260 265				
ata tta gca naa atn tcg aga ggc ncg gat aaa gaa cgc gta tta tct	1167			
Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser				
270 275 280				
ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc	1215			
Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe				
285 290 295				
aaa tat caa gtc tat taactattga atttttgcaa atgagataag agtatagtgc	1270			
Lys Tyr Gln Val Tyr				
300				
tgattttcttc aaagcgaaaa ggaggaaata gcttggttcta atttattaca ataatgggttg	1330			
tattcatctt gattttgaag gaaagagagt gttttttgta taaaagcatt ttcgtcacct	1390			
aaatttacta atcctccaaa ttctcctcct cgnagaatth ctttcggacc ggtagggcag	1450			
tccatggata ttacaggtgt accgcaagcc atgcttttcta ggataactgt cggtaacccc	1510			
tctttcaaag aggtgtgtaa aaatagctta gcatttttta ttaatggata cggattatct	1570			

ttatttccta aaagaaaaca atcttcttgt agattgagtg attctatttg tttctctaata 1630
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<210> 36
 <211> 302
 <212> PRT
 <213> Pasteurella multocida

<400> 36
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 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
 35 40 45
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
 85 90 95
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
 100 105 110
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
 115 120 125
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
 130 135 140
 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
 145 150 155 160
 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
 165 170 175
 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
 180 185 190
 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
 195 200 205
 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly
 210 215 220
 Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
 225 230 235 240
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
 245 250 255
 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg
 260 265 270
 Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala

275		280		285
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr				
290		295		300

<210> 37
 <211> 2029
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (2)..(499)

<220>
 <223> mglB

<220>
 <223> Nucleotides at positions 98, 296 and 302 are A, T, G, or C. The corresponding amino acids are unknown.

<220>
 <223> Nucleotides at positions 928, 1007, 1740, 1808, 1816, and 1820 are A, T, G, or C.

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gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97
 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
 20 25 30

nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145
 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
 35 40 45

tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193
 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
 50 55 60

tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241
 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
 65 70 75 80

gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289
 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
 85 90 95

atc ttc ngg gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337
 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
 100 105 110

ggt gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385
 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
 115 120 125

gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act 433
 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
 130 135 140

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gaa ggc aca aaa tgg cag tta aaa cga tgc tgt cct acg tat ccc tta 481
Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
145 150 155 160

tgt tgg tgt gga tgc gga taacttaaag gagttcctaa aataataaac 529
Cys Trp Cys Gly Cys Gly
165

tataacaaaa caagamgttg taattctcgg ggagggtatac cctccccctt tttatgtgag 589
gttggatatg acaactcaaa ttccaaatca agacagtga atactgctca caatgaccaa 649
cgtctgtaaa tcctttcccg gtgttaaagc gttagacaat gcaaacctaa ctgtgcgctc 709
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gtatcgacat tgggtcgaaa tatgaaattt atcagctgat tatggagtta gccaaaaaag 1969
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<210> 38
<211> 166
<212> PRT
<213> Pasteurella multocida

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 20 25 30
 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
 35 40 45
 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
 50 55 60
 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
 65 70 75 80
 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
 85 90 95
 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
 100 105 110
 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
 115 120 125
 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
 130 135 140
 Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
 145 150 155 160
 Cys Trp Cys Gly Cys Gly
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<210> 39
 <211> 2628
 <212> DNA
 <213> Pasteurella multocida

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 <222> (326)..(766)

<220>
 <223> mioC

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 tcaattggaa attgatgaat taaaagaaaa aaataaccaa tctcaacaag caaatgacgc 180
 attacgcagt gaaaatgaac aactaaagag tgagcaccaa aactggcaag aacgttttacg 240
 ctcattatta ggcaaaattg ataacgtata attcacttct tattaaggct tagtttttct 300
 aagccttatt ttttaggaga aatta atg aaa aca aaa att tgt att atc act 352
 Met Lys Thr Lys Ile Cys Ile Ile Thr
 1 5
 ggc agt acg ctt ggt ggt gca gaa tat gtt gca gaa cat att gct gaa 400

Gly 10	Ser	Thr	Leu	Gly 15	Ala	Glu	Tyr	Val	Ala 20	Glu	His	Ile	Ala	Glu 25				
ata Ile	tta Leu	gaa Glu	caa Gln	caa Gln 30	gat Asp	tat Tyr	cct Pro	gta Val	cgt Arg 35	tta Leu	gaa Glu	cat His	gga Gly	cca Pro 40	aas Asn	448		
ttt Phe	gaa Glu	gaa Glu	gtg Val 45	atc Ile	gat Asp	gaa Glu	aaa Lys	tgt Cys 50	tgg Trp	ctt Leu	gtt Val	gtc Val	acc Thr 55	tct Ser	acc Thr	496		
cat His	ggg Gly	gca Ala 60	ggg Gly	gaa Glu	tta Leu	ccg Pro	gat Asp 65	aat Asn	att Ile	aaa Lys	cct Pro	ctg Leu 70	ttt Phe	gaa Glu	aaa Lys	544		
tta Leu	gca Ala 75	ttt Phe	cac His	cca Pro	aaa Lys	cag Gln 80	tta Leu	gct Ala	gac Asp	tta Leu	cgc Arg 85	ttt Phe	gcg Ala	gtg Val	atc Ile	592		
ggg Gly 90	tta Leu	ggg Gly	aat Asn	tcg Ser 95	gat Asp	tat Tyr	gat Asp	acc Thr	ttc Phe	tgt Cys 100	cac His	gca Ala	gtg Val	gat Asp 105	cat His	640		
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tccctgaata				agattgaatg			ttttttattc			tgtggataac			taaagaagtt			attcacagtt		966
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<210> 40
 <211> 147
 <212> PRT
 <213> Pasteurella multocida

<400> 40
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 20 25 30
 Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu
 35 40 45
 Lys Cys Trp Leu Val Val Thr Ser Thr His Gly Ala Gly Glu Leu Pro
 50 55 60
 Asp Asn Ile Lys Pro Leu Phe Glu Lys Leu Ala Phe His Pro Lys Gln
 65 70 75 80
 Leu Ala Asp Leu Arg Phe Ala Val Ile Gly Leu Gly Asn Ser Asp Tyr
 85 90 95
 Asp Thr Phe Cys His Ala Val Asp His Val Glu Gln Leu Leu Leu Ser
 100 105 110
 Lys Asp Ala Leu Gln Leu Cys Glu Ser Leu Arg Met Asp Met Leu Thr

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Ile Thr Asp Pro Glu His Thr Ala Glu Gln Trp	Leu Pro Gln Phe Leu	
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Ser Gln Leu
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<210> 41
<211> 5191
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<220>
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<220>
<223> mreB

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Met Leu Phe Lys Lys Ile Arg Gly Leu Phe	
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Ser Asn Asp Leu Ser Ile Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr	
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gtc aaa gga caa ggg att gtt tta gat gaa cct tct gtt gtg gcg att	3328
Val Lys Gly Gln Gly Ile Val Leu Asp Glu Pro Ser Val Val Ala Ile	
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Arg Gln Glu Arg Ser Gly Ala Leu Lys Ser Ile Ala Val Gly Arg	
45 50 55	
gat gcc aaa tta atg tta ggc cgt aca ccg aaa agc att gca gcg att	3424
Asp Ala Lys Leu Met Leu Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile	
60 65 70	
cgt cct atg aaa gat ggg gtg atc gca gat ttc ttt gtg aca gaa aaa	3472
Arg Pro Met Lys Asp Gly Val Ile Ala Asp Phe Phe Val Thr Glu Lys	
75 80 85 90	
atg ttg caa tat ttt att aaa caa gtg cac agc agc aat ttt atg cgt	3520
Met Leu Gln Tyr Phe Ile Lys Gln Val His Ser Ser Asn Phe Met Arg	
95 100 105	
cca agt cca cgt gtc tta gtt tgt gta cct gcg gga gct acg caa gtc	3568
Pro Ser Pro Arg Val Leu Val Cys Val Pro Ala Gly Ala Thr Gln Val	
110 115 120	
gaa cga cgt gca atc aaa gaa tct gcc att ggt gct ggg gca cgc gag	3616
Glu Arg Arg Ala Ile Lys Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu	
125 130 135	
gtg tac ttg att gag gaa ccg atg gcg gca gcg att ggt gct aaa tta	3664
Val Tyr Leu Ile Glu Glu Pro Met Ala Ala Ala Ile Gly Ala Lys Leu	
140 145 150	
cct gtt tcg act gcc aca ggt tcg atg gtg atc gat atc ggt ggt ggt	3712
Pro Val Ser Thr Ala Thr Gly Ser Met Val Ile Asp Ile Gly Gly Gly	
155 160 165 170	
acg acg gaa gtt gcg gtg att tct tta aat ggc att gtg tat tcc tct	3760
Thr Thr Glu Val Ala Val Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser	
175 180 185	
tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat	3808
Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr	
190 195 200	
gta cgc aag acg ttc ggt tca att att ggg gaa ccg aca gca gag cgt	3856
Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg	
205 210 215	
atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc	3904
Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val	
220 225 230	
cgt gaa att gaa gtg cat ggt cat aac tta gca gaa ggt gcg ccg cgt	3952
Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg	
235 240 245 250	

tct ttc aaa ctc acc tca cgt gat gtg tta gaa gct att caa gcc ccg	4000
Ser Phe Lys Leu Thr Ser Arg Asp Val Leu Glu Ala Ile Gln Ala Pro	
255 260 265	
tta aat ggc att gtt gcg gca gtg cgc acg gcc ttg gaa gag tgt caa	4048
Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln	
270 275 280	
cca gaa cat gct gcg gat att ttt gaa cgt ggc atg gtc tta act ggt	4096
Pro Glu His Ala Ala Asp Ile Phe Glu Arg Gly Met Val Leu Thr Gly	
285 290 295	
ggc ggt gcc ctt att cgt aat att gat gtt tta ctg tca aaa gaa acc	4144
Gly Gly Ala Leu Ile Arg Asn Ile Asp Val Leu Ser Lys Glu Thr	
300 305 310	
ggg gtg ccg gtt atc atc gcc gat gat cct tta acc tgt gtt gcc cgt	4192
Gly Val Pro Val Ile Ile Ala Asp Asp Pro Leu Thr Cys Val Ala Arg	
315 320 325 330	
ggg ggt ggc gag gca tta gag atg atc gat atg cac ggt ggt gat att	4240
Gly Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile	
335 340 345	
ttt agt gac gat atc taatatgatt taaaagtgcg gtgatattag accgcacttt	4295
Phe Ser Asp Asp Ile	
350	
tacttctctt ttattgctga caaggctagc ctaattcgta tatgaaacct atttttggaa	4355
aagcacctcc tttaggtctt cgcttaattc tggcgatttt agcatccatt gcattgattg	4415
tttcggacgg tcaatccaat gcgatgatta aagcacgcag tattatggaa accgcagtag	4475
gcgggctgta ttatcttgcc aatacaccga gaacggtatt ggatgggggt tcagataatt	4535
tggttgatac caataaattg caaattgaaa accgagtttt gcgtgatcaa ctgcgtgaaa	4595
aaaatgcaga ttatttggtg ttagatcaac tcaaagtaga aaatcaacgc ctgcgcttat	4655
tgcttaattc ccctctacgt acagatgagt ataaaaaat tgctgaagtt ttaacggcag	4715
aaactgatgt gtatcgtaag caagtcgtga ttaaccaagg acaacgtgac ggtgcttatg	4775
tcgggcagcc gattattgat gaaaagggtg ttggtgggca acttatctcc gttggtgaaa	4835
atacgagtgc cgctcttcta ttgacagatg tgactcattc tattccagta caagtactac	4895
gtaatgatgt ccgtttgatt gctagtggaa caggacggaa tgatgaactg agtttagatc	4955
atgtgccgcg ttcggtcgat attgtcaaag gggatttatt agtcacttct ggattaggtg	5015
ggcgtttttt agaaggttat cctggtgcca ttgtggaatc cgtatcacgt gatgggcaaa	5075
attattttgc tactgtaaca gcaaagccat tagcttcgat tgaacgttta cgctatgttt	5135
tgcttttatg gccgacgaat gaagagatgc gcaaagtcca gtctatttca cctgca	5191

<210> 42
 <211> 351
 <212> PRT
 <213> Pasteurella multocida

<400> 42
Met Leu Phe Lys Lys Ile Arg Gly Leu Phe Ser Asn Asp Leu Ser Ile
1 5 10 15
Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr Val Lys Gly Gln Gly Ile
20 25 30
Val Leu Asp Glu Pro Ser Val Val Ala Ile Arg Gln Glu Arg Ser Gly
35 40 45
Ala Leu Lys Ser Ile Ala Ala Val Gly Arg Asp Ala Lys Leu Met Leu
50 55 60
Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile Arg Pro Met Lys Asp Gly
65 70 75 80
Val Ile Ala Asp Phe Phe Val Thr Glu Lys Met Leu Gln Tyr Phe Ile
85 90 95
Lys Gln Val His Ser Ser Asn Phe Met Arg Pro Ser Pro Arg Val Leu
100 105 110
Val Cys Val Pro Ala Gly Ala Thr Gln Val Glu Arg Arg Ala Ile Lys
115 120 125
Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu Val Tyr Leu Ile Glu Glu
130 135 140
Pro Met Ala Ala Ala Ile Gly Ala Lys Leu Pro Val Ser Thr Ala Thr
145 150 155 160
Gly Ser Met Val Ile Asp Ile Gly Gly Gly Thr Thr Glu Val Ala Val
165 170 175
Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser Ser Val Arg Ile Gly Gly
180 185 190
Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr Val Arg Lys Thr Phe Gly
195 200 205
Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg Ile Lys Gln Glu Ile Gly
210 215 220
Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His
225 230 235 240
Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser
245 250 255
Arg Asp Val Leu Glu Ala Ile Gln Ala Pro Leu Asn Gly Ile Val Ala
260 265 270
Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp
275 280 285
Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Gly Ala Leu Ile Arg
290 295 300
Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile
305 310 315 320
Ala Asp Asp Pro Leu Thr Cys Val Ala Arg Gly Gly Gly Glu Ala Leu
325 330 335

Glu Met Ile Asp Met His Gly Gly Asp Ile Phe Ser Asp Asp Ile
340 345 350

<210> 43
<211> 2172
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(1464)

<220>
<223> pnp

<400> 43
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Thr Arg Val Gly Ile Gly Trp His Leu Asn Pro Asn Thr Ala Leu Ile
1 5 10 15

gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc gaa gca tac cgt 96
Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
20 25 30

atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct 144
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
35 40 45

gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc 192
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
50 55 60

agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc 240
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
65 70 75 80

gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca 288
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
85 90 95

gtg gat act gtt cgt gca tta gat att tgt act ggt gtt tta cca cgt 336
Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
100 105 110

aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct 384
Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
115 120 125

gtc gcg aca tta ggt aca gaa cgt gat gca caa att att gat gaa tta 432
Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
130 135 140

aca ggt gag cgt tca gat cac ttc tta ttc cac tac aac ttc ccg cca 480
Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
145 150 155 160

tat tct gtg ggt gaa acc ggt atg att ggt tca cca aaa cgt cgt gaa 528
Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
165 170 175

att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct gca gtg atg cca 576
Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro

			180				185				190						
aca Thr	ctt Leu	gcc Ala 195	gag Glu	ttc Phe	ccg Pro	tat Tyr	gtg Val 200	gta Val	cgt Arg	gtt Val	gtc Val	tct Ser 205	gaa Glu	atc Ile	aca Thr	624	
gaa Glu	tca Ser 210	aat Asn	ggg Gly	tct Ser	tct Ser 215	tct Ser	atg Met	gca Ala	tcg Ser	gtt Val	tgt Cys 220	ggg Gly	gcg Ala	tct Ser	tta Leu	672	
gca Ala 225	tta Leu	atg Met	gat Asp	gcg Ala	ggg Gly 230	gta Val	cca Pro	att Ile	aaa Lys	gcg Ala 235	gcg Ala	gtt Val	gca Ala	ggg Gly	att Ile 240	720	
gca Ala	atg Met	ggc Gly	tta Leu	gtc Val 245	aaa Lys	gaa Glu	gac Asp	gaa Glu	aaa Lys 250	ttt Phe	gtg Val	gtg Val	ctt Leu	tca Ser 255	gac Asp	768	
atc Ile	tta Leu	ggg Gly	gat Asp 260	gaa Glu	gat Asp	cac His	tta Leu	ggg Gly 265	gac Asp	atg Met	gac Asp	ttc Phe 270	aaa Lys	gtc Val	gcg Ala	816	
ggg Gly	aca Thr	cgt Arg 275	acg Thr	ggg Gly	gtg Val	acg Thr	gca Ala 280	tta Leu	caa Gln	atg Met	gat Asp	atc Ile 285	aaa Lys	atc Ile	gaa Glu	864	
ggg Gly	atc Ile 290	aca Thr	gca Ala	gaa Glu	atc Ile	atg Met 295	caa Gln	att Ile	gcg Ala	tta Leu	aac Asn 300	caa Gln	gcg Ala	aaa Lys	agc Ser	912	
gca Ala 305	cgt Arg	tta Leu	cac His	att Ile	tta Leu 310	ggg Gly	gtg Val	atg Met	gag Glu	caa Gln 315	gcg Ala	atc Ile	cca Pro	gcg Ala	cca Pro 320	960	
cgt Arg	gcg Ala	gat Asp	att Ile	tct Ser 325	gat Asp	ttt Phe	gca Ala	ccg Pro	cgt Arg 330	att Ile	tac Tyr	act Thr	atg Met	aaa Lys 335	att Ile	1008	
gat Asp	ccg Pro	aag Lys	aaa Lys 340	atc Ile	aaa Lys	gat Asp	gtg Val	atc Ile 345	ggg Gly	aaa Lys	ggg Gly	ggg Gly	gca Ala 350	acc Thr	att Ile	1056	
cgt Arg	gcc Ala	tta Leu 355	aca Thr	gaa Glu	gaa Glu	aca Thr	ggg Gly 360	acc Thr	tca Ser	att Ile	gat Asp	atc Ile 365	gat Asp	gat Asp	gat Asp	1104	
ggg Gly	acg Thr 370	gtg Val	aag Lys	att Ile	gct Ala	gcg Ala 375	ggt Val	gat Asp	ggc Gly	aat Asn	tca Ser 380	gca Ala	aaa Lys	gag Glu	gtg Val	1152	
atg Met 385	gcg Ala	cgt Arg	att Ile	gaa Glu	gat Asp 390	att Ile	act Thr	gca Ala	gaa Glu	gtt Val 395	gaa Glu	gcg Ala	ggg Gly	gca Ala	gtg Val 400	1200	
tat Tyr	aaa Lys	ggg Gly	aaa Lys	ggt Val 405	act Thr	cgt Arg	tta Leu	gct Ala	gat Asp 410	ttt Phe	ggg Gly	gcc Ala	ttc Phe	ggt Val 415	tct Ser	1248	
atc Ile	gta Val	ggg Gly	aac Asn 420	aaa Lys	gaa Glu	ggc Gly	tta Leu	gtg Val 425	cat His	att Ile	tct Ser	caa Gln	atc Ile 430	gcg Ala	gaa Glu	1296	
gag	cgt	gtt	gag	aaa	gtg	agt	gat	tat	ctt	gca	gtg	ggg	caa	gaa	gtg	1344	

Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
435 440 445

act gtt aaa gtg gtt gag att gat cgt caa ggt cgt att cgt tta acc 1392
Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
450 455 460

atg aaa gaa gtt gca cca aag caa gaa cac gtt gat tct gtt gtc gca 1440
Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465 470 475 480

gac gtt gcc gca gaa gaa aac gca taagcaataa acaccaacgc ccttcgtgat 1494
Asp Val Ala Ala Glu Glu Asn Ala
485

aaagggcggtt ggtgtgcatg ttgataagta caatttgtgc ttttaaggcga agcgaaatga 1554
agcaatttca tccgtgggtta aagtgcctgc taattttccc attttgggta tgttgtttta 1614
cagcttgtgt taatcatgaa caagtttttc tttcaaaaga gaaattaatg ttagcagagc 1674
aacatccgaa tgatcatctt gagcatgagg tgatgggtgc gcaaattagc gaattgttac 1734
ttgttaaagg gttaaaaaa gaagaacgtg cgattttaca ttttgagcga ggcgtgctgt 1794
acgatagctt aggattgtgg gcattggcgc gttatgattt tgaccaaaca ttagcgttgt 1854
atccaaagtt ggcagcagcg ttttaattatt taggtttata tttattgtta gaggaagatt 1914
acagcgcatac tctagatatac tttaatgtgt tgtttgaact tgatcctcaa tatgagtatg 1974
cattcctaaa tagagggcta aatttttatt acgtcggacg ttatgaatta gctcagcggg 2034
attttcttca attttatcaa gccgataaat cagatccata ccgcacttta tggctttatt 2094
taaatagaatt aaagcataat cctcaggatg cttctaaaaa tcttgctcaa cgagcaatgg 2154
ggctttctga tgaatatt 2172

<210> 44
<211> 488
<212> PRT
<213> Pasteurella multocida

<400> 44
Thr Arg Val Gly Ile Gly Trp His Leu Asn Pro Asn Thr Ala Leu Ile
1 5 10 15
Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
20 25 30
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
35 40 45
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
50 55 60
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
65 70 75 80
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
85 90 95

Val	Asp	Thr	Val	Arg	Ala	Leu	Asp	Ile	Cys	Thr	Gly	Val	Leu	Pro	Arg	
			100					105					110			
Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg	Gly	Glu	Thr	Gln	Ala	Leu	Ala	
		115					120					125				
Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	Ala	Gln	Ile	Ile	Asp	Glu	Leu	
	130					135					140					
Thr	Gly	Glu	Arg	Ser	Asp	His	Phe	Leu	Phe	His	Tyr	Asn	Phe	Pro	Pro	
145					150					155					160	
Tyr	Ser	Val	Gly	Glu	Thr	Gly	Met	Ile	Gly	Ser	Pro	Lys	Arg	Arg	Glu	
			165						170					175		
Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg	Gly	Val	Ala	Ala	Val	Met	Pro	
			180					185					190			
Thr	Leu	Ala	Glu	Phe	Pro	Tyr	Val	Val	Arg	Val	Val	Ser	Glu	Ile	Thr	
	195						200					205				
Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala	Ser	Val	Cys	Gly	Ala	Ser	Leu	
	210					215					220					
Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile	Lys	Ala	Ala	Val	Ala	Gly	Ile	
225					230					235					240	
Ala	Met	Gly	Leu	Val	Lys	Glu	Asp	Glu	Lys	Phe	Val	Val	Leu	Ser	Asp	
			245					250						255		
Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly	Asp	Met	Asp	Phe	Lys	Val	Ala	
		260						265					270			
Gly	Thr	Arg	Thr	Gly	Val	Thr	Ala	Leu	Gln	Met	Asp	Ile	Lys	Ile	Glu	
	275						280					285				
Gly	Ile	Thr	Ala	Glu	Ile	Met	Gln	Ile	Ala	Leu	Asn	Gln	Ala	Lys	Ser	
	290					295					300					
Ala	Arg	Leu	His	Ile	Leu	Gly	Val	Met	Glu	Gln	Ala	Ile	Pro	Ala	Pro	
305					310					315					320	
Arg	Ala	Asp	Ile	Ser	Asp	Phe	Ala	Pro	Arg	Ile	Tyr	Thr	Met	Lys	Ile	
			325						330					335		
Asp	Pro	Lys	Lys	Ile	Lys	Asp	Val	Ile	Gly	Lys	Gly	Gly	Ala	Thr	Ile	
		340					345						350			
Arg	Ala	Leu	Thr	Glu	Glu	Thr	Gly	Thr	Ser	Ile	Asp	Ile	Asp	Asp	Asp	
	355						360					365				
Gly	Thr	Val	Lys	Ile	Ala	Ala	Val	Asp	Gly	Asn	Ser	Ala	Lys	Glu	Val	
	370					375					380					
Met	Ala	Arg	Ile	Glu	Asp	Ile	Thr	Ala	Glu	Val	Glu	Ala	Gly	Ala	Val	
385					390					395					400	
Tyr	Lys	Gly	Lys	Val	Thr	Arg	Leu	Ala	Asp	Phe	Gly	Ala	Phe	Val	Ser	
			405						410				415			
Ile	Val	Gly	Asn	Lys	Glu	Gly	Leu	Val	His	Ile	Ser	Gln	Ile	Ala	Glu	
		420						425					430			

Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
435 440 445

Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
450 455 460

Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465 470 475 480

Asp Val Ala Ala Glu Glu Asn Ala
485

<210> 45
<211> 633
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (2)..(631)

<220>
<223> purF

<400> 45
c gat ggg gtt tct gtt tat gct gcc cgt gtt cat atg gga caa cgt tta 49
Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu
1 5 10 15

ggt gaa aaa att gca cgg gaa tgg gcg gat gtg gat gat att gat gtg 97
Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
20 25 30

gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg 145
Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
35 40 45

cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat 193
Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
50 55 60

gta gga cgt acg ttt att atg ccg ggg cag gca ttg cga gtc agt tct 241
Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
65 70 75 80

gtt aga cgt aaa ctc aat acc att gct tca gaa ttt aaa gat aag aat 289
Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn
85 90 95

gtg tta tta gtt gac gac tcg att gta cgt ggt acc acg tct gaa caa 337
Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln
100 105 110

att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc 385
Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
115 120 125

tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg 433
Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
130 135 140

cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att 481

Pro	Thr	Lys	Asn	Glu	Leu	Ile	Ala	Tyr	Gly	Arg	Asp	Val	Asp	Glu	Ile		
145					150					155					160		
gct	aac	tta	att	ggg	gtg	gat	aaa	ttg	att	ttc	caa	gat	ttg	gat	gcg	529	
Ala	Asn	Leu	Ile	Gly	Val	Asp	Lys	Leu	Ile	Phe	Gln	Asp	Leu	Asp	Ala		
				165					170					175			
tta	act	ggg	tct	gtg	caa	caa	gaa	aat	cca	agt	att	caa	gac	ttt	gat	577	
Leu	Thr	Gly	Ser	Val	Gln	Gln	Glu	Asn	Pro	Ser	Ile	Gln	Asp	Phe	Asp		
			180					185					190				
tgt	tcg	gtg	ttt	aca	ggg	gtt	tat	gtg	acg	ggc	gat	att	aca	cct	gaa	625	
Cys	Ser	Val	Phe	Thr	Gly	Val	Tyr	Val	Thr	Gly	Asp	Ile	Thr	Pro	Glu		
		195					200					205					
tat	ctg	ga														633	
Tyr	Leu																
	210																

<210> 46
 <211> 210
 <212> PRT
 <213> Pasteurella multocida

<400> 46
 Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu
 1 5 10 15
 Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
 20 25 30
 Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
 35 40 45
 Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
 50 55 60
 Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
 65 70 75 80
 Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn
 85 90 95
 Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln
 100 105 110
 Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
 115 120 125
 Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
 130 135 140
 Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
 145 150 155 160
 Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
 165 170 175
 Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
 180 185 190
 Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu

195	200	205	
Tyr Leu			
210			
<210> 47			
<211> 4788			
<212> DNA			
<213> Pasteurella multocida			
<220>			
<221> CDS			
<222> (1)..(876)			
<220>			
<223> rci			
<220>			
<223> Nucleotide at position 3084 is A, T, G, or C.			
<400> 47			
gac gag gag aga aaa tta gct gat ttg gca aaa ggt atc gct cca gat			48
Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp			
1 5 10 15			
att att ttt aga gat gta ata gaa cgc tat caa aat gaa gtg tct ata			96
Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile			
20 25 30			
act aaa aaa ggc gcg cga aat gaa att ata aga tta aac cgc ttt tta			144
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu			
35 40 45			
aga tat gat att tct aat ctg tat att cgt gat tta aga aaa gaa gat			192
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp			
50 55 60			
ttt gag gag tgg atc aga att cgc cta acc gaa gta tcg gat gct agc			240
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser			
65 70 75 80			
gtt aga cgt gag ctt gtt act ata tcg tca gtg ctg aca aca gca ata			288
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile			
85 90 95			
aat aag tgg gga tat att tca agg cat cca atg act ggt att gaa aaa			336
Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys			
100 105 110			
cca aaa aac tcg gca gaa aga aaa gaa cga tat tca gaa cag gac att			384
Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile			
115 120 125			
aaa aca ata tta gaa aca gct aga tat tgt gaa gat aaa cta ccc ata			432
Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile			
130 135 140			
aca ctc aaa caa aga gta gca att gca atg tta ttt gct att gaa acc			480
Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr			
145 150 155 160			
gct atg cgt gct ggt gag att gct agt ata aaa tgg gat aat gtt ttt			528

[illegible]

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tcttgctctt gccaatgtga aatacacctt gatataagaa agtggtgaac ggaaagaact 1876
ttgaataatc agcagttaca tatcctttac ttccatttct aagcacaact ggctcaccgg 1936
ttaatgcttt ttctaagtca aatgctttca ttttttactc tccagcttgc tcatcaataa 1996
gctcatcaat ccattctcga atttcagatt ggaaattttc taacgaatta ttttcattaa 2056
aataatctgc ttcttttaac ttactcacgg ctggttttact aaagcattta taaaaagac 2116
gctttttctc aaacaaatca tcttttgaga ttgcgcatac ttttctacg ccctctatac 2176
ttttgtcttg aataaaaacta ttaaaaagaa cctcttcttg ctgcttggtt tctactaaaa 2236
tagaaatcgt atattttttt ggatattcca tttttaatcc tttcttttag ataacaaaaa 2296
accgcatttc tgcggttatt ctgtgtattt atttaaaata ttacttatag tttcagcatc 2356
ttctaagtgt aatttagaat agcttgaggt catttttctt ttaacggcaa tctcaattc 2416
ttccagcttt aagctataca agtagtcttt tttatcttta taaatacgac cgtacaccat 2476
tccggataat ttaccttctt cataccatt agataaattg atctttctat ctgcaccgag 2536
cactetaatt gttaaattt ttcttccaat ttttaagact tcagcctcat gttcaatgtt 2596
tgagcgcag agtggttcta aaaaatatac ggtatcgcca actttaagat ttttaatcca 2656
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gaatcggttg ccagtgtgta acgttaatag ctagatcata aattggacca ttctgattta 3256
tagctacca aaaatattca ccatcagcaa tttctcttga tgcaattgag taatgctcgc 3316
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cactaatcca gttgctatat tcccaatgaa aattaagctt ctcatagcca ttgatgactt 3436
gatctaacgc aggtcttaat tgggtttctc caacaataat atgtgtgtt atcttaattc 3496
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tctcatgat aaattccatg tttatttacc ttttttctgg cacaaaaaa cagctattg 3676

cgtgctgtct tgattgatat aatcaattaa tctaagccca atccatttca taactggaac 3736
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gttgcgatat gggatttttag tgtaatcgtc tggaaatccc tgtaatcttt cacactcacg 3856
cggcgttagt tttctaacaa ctgattctac tgataaagca acgcaaggaa cattattacc 3916
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agcaagaact ccaccgcttg ctcttaatgt tcccgaaca tcggatttgc gatattgagc 4156
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cacaagaaac actcttttac gacgttgggc aactccgaag tattgagcat cgagaactcg 4336
ccagcagatt gttcggattg aatgcacata accagcgttc gtccatcttc tccctgtgtg 4396
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gggtggatagc acaccgggaa cgttttccca cacgagaatg cacggtgggtt tgttgtcatt 4516
gaatctaaca tagtcgatcg cttctaaaat ttttaattaa actaacgtga gatttcctcg 4576
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aactaaaacg tctggtgccg gaatttcacg atctaataatt ttctgttgca attcagtcatt 4696
atcaccaaga ttgggaacgt tagggtaatg gtaagctaatt actgcgcttg ggaattgctc 4756
aatttcagaa aaccagagtg gctctgcgaa tt 4788

<210> 48
<211> 292
<212> PRT
<213> Pasteurella multocida

<400> 48
Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp
1 5 10 15
Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
20 25 30
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
35 40 45
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
50 55 60
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
65 70 75 80
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
85 90 95

Asn	Lys	Trp	Gly	Tyr	Ile	Ser	Arg	His	Pro	Met	Thr	Gly	Ile	Glu	Lys	
			100					105					110			
Pro	Lys	Asn	Ser	Ala	Glu	Arg	Lys	Glu	Arg	Tyr	Ser	Glu	Gln	Asp	Ile	
		115					120					125				
Lys	Thr	Ile	Leu	Glu	Thr	Ala	Arg	Tyr	Cys	Glu	Asp	Lys	Leu	Pro	Ile	
	130					135					140					
Thr	Leu	Lys	Gln	Arg	Val	Ala	Ile	Ala	Met	Leu	Phe	Ala	Ile	Glu	Thr	
145					150					155					160	
Ala	Met	Arg	Ala	Gly	Glu	Ile	Ala	Ser	Ile	Lys	Trp	Asp	Asn	Val	Phe	
				165					170					175		
Leu	Glu	Lys	Arg	Ile	Val	His	Leu	Pro	Thr	Thr	Lys	Asn	Gly	His	Ser	
			180					185					190			
Arg	Asp	Val	Pro	Leu	Ser	Gln	Arg	Ala	Val	Ala	Leu	Ile	Leu	Lys	Met	
		195					200					205				
Lys	Glu	Val	Glu	Asn	Gly	Asp	Leu	Val	Phe	Gln	Thr	Thr	Pro	Glu	Ser	
	210					215					220					
Leu	Ser	Thr	Thr	Phe	Arg	Val	Leu	Lys	Lys	Glu	Cys	Gly	Leu	Glu	His	
225					230					235					240	
Leu	His	Phe	His	Asp	Thr	Arg	Arg	Glu	Ala	Leu	Thr	Arg	Leu	Ser	Lys	
				245					250					255		
Lys	Val	Asp	Val	Met	Thr	Leu	Ala	Lys	Ile	Ser	Gly	His	Arg	Asp	Leu	
			260					265					270			
Arg	Ile	Leu	Gln	Asn	Thr	Tyr	Tyr	Ala	Pro	Asn	Met	Ser	Glu	Val	Ala	
		275					280					285				
Asn	Leu	Leu	Asp													
		290														

<210> 49
 <211> 1618
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (2)..(1195)

<220>
 <223> sopE

<400> 49
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 Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile
 1 5 10 15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt 97
 Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly
 20 25 30

att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat 145
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn

35	40	45	
gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly 50 55 60			193
aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val 65 70 75 80			241
aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp 85 90 95			289
gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile 100 105 110			337
aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys 115 120 125			385
aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp 130 135 140			433
aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn 145 150 155 160			481
gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala 165 170 175			529
gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met 180 185 190			577
ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp 195 200 205			625
tat gcc gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa Tyr Ala Val Thr Arg Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu 210 215 220			673
cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser 225 230 235 240			721
ggt gtc aca caa cca ctc tat ttt gac att aac gac agc tcg act gat Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp 245 250 255			769
gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn 260 265 270			817
ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe 275 280 285			865
aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att			913

Lys	Phe	Glu	Val	Tyr	Thr	Arg	Thr	Ala	Gln	Ile	Leu	Lys	Asp	Thr	Ile		
290						295					300						
gca	ggg	gcg	ttt	gat	tgg	gca	gtg	gat	aaa	gat	att	tct	gtc	acg	cta	961	
Ala	Gly	Ala	Phe	Asp	Trp	Ala	Val	Asp	Lys	Asp	Ile	Ser	Val	Thr	Leu		
305					310					315					320		
gtg	aaa	gat	att	att	gaa	gca	atc	aat	gcg	aag	tgg	cgt	gat	tac	acc	1009	
Val	Lys	Asp	Ile	Ile	Glu	Ala	Ile	Asn	Ala	Lys	Trp	Arg	Asp	Tyr	Thr		
				325					330					335			
aca	aaa	ggc	tac	tta	att	ggc	ggg	aaa	gcg	tgg	ctt	aat	aaa	gag	ctt	1057	
Thr	Lys	Gly	Tyr	Leu	Ile	Gly	Gly	Lys	Ala	Trp	Leu	Asn	Lys	Glu	Leu		
			340					345					350				
aac	agt	gca	acg	aat	tta	aaa	gat	gcg	aag	ttg	ttg	atc	tct	tat	gat	1105	
Asn	Ser	Ala	Thr	Asn	Leu	Lys	Asp	Ala	Lys	Leu	Leu	Ile	Ser	Tyr	Asp		
		355					360					365					
tat	cac	cca	gta	cca	ccg	ctc	gaa	cag	cta	ggc	ttt	aat	cag	tac	att	1153	
Tyr	His	Pro	Val	Pro	Pro	Leu	Glu	Gln	Leu	Gly	Phe	Asn	Gln	Tyr	Ile		
		370				375					380						
tct	gat	gaa	tac	ctt	gtt	gat	ttt	tca	aat	cgt	tta	gca	tcg			1195	
Ser	Asp	Glu	Tyr	Leu	Val	Asp	Phe	Ser	Asn	Arg	Leu	Ala	Ser				
385					390					395							
taaggggtag aaaatggctt taccacgcaa acttaaattg atgaatttaa tcatcgacgg																1255	
taacaaatat ctcggcgaag tcacggaagt gactcaacca aaattagcaa tgaaaatcga																1315	
agaatttcgc gcgggcggta tgattgggtc ggtggatgtc aatctcgggc ttgaaaagct																1375	
cgaagcggaa tttaaagccg gtggctacat ggtcgaatta attaaaaaat tcggcgggtc																1435	
aatcaacggc attccattgc gttttcttgg ctcatatcag cgtgatgaca cagaagaagt																1495	
cacatctgtt gagcttgtga tgcaaggtcg atttactgaa attgacagcg gaaacagcaa																1555	
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tga																1618	

<210> 50
 <211> 398
 <212> PRT
 <213> Pasteurella multocida

<400> 50																	
Gly	Asp	Leu	Cys	Leu	Lys	Ile	Ser	Thr	Trp	Cys	Gln	Ser	His	Arg	Ile		
1				5					10					15			
Asn	Gln	Ala	Ile	Arg	Thr	Ile	Gln	Ser	Leu	Ser	Thr	Ala	Val	Ile	Gly		
			20					25					30				
Ile	Val	Cys	Thr	Ala	Asn	Asp	Ala	Asp	Asn	Glu	Thr	Phe	Pro	Leu	Asn		
		35					40					45					
Glu	Pro	Val	Leu	Ile	Thr	Asn	Val	Ala	Ala	Ala	Ile	Gly	Lys	Ala	Gly		
	50					55					60						
Lys	Gln	Gly	Thr	Leu	Ser	Arg	Ala	Leu	Asp	Gly	Ile	Ser	Asp	Val	Val		

65					70						75				80
Asn	Cys	Lys	Val	Ile	Val	Val	Arg	Val	Gln	Glu	Ser	Ala	Gln	Glu	Asp
				85					90					95	
Glu	Glu	Thr	Lys	Ala	Ser	Glu	Met	Asn	Thr	Ala	Ile	Ile	Gly	Thr	Ile
			100					105					110		
Thr	Glu	Glu	Gly	Gln	Tyr	Thr	Gly	Leu	Lys	Ala	Leu	Leu	Ile	Ala	Lys
			115				120						125		
Asn	Lys	Phe	Gly	Ile	Lys	Pro	Arg	Ile	Leu	Cys	Val	Pro	Lys	Phe	Asp
	130					135					140				
Thr	Lys	Glu	Val	Ala	Thr	Glu	Leu	Ala	Ser	Ile	Ala	Ala	Lys	Leu	Asn
	145				150					155					160
Ala	Phe	Ala	Tyr	Ile	Ser	Cys	Gln	Gly	Cys	Lys	Thr	Lys	Glu	Gln	Ala
				165					170					175	
Val	Gln	Tyr	Lys	Arg	Asn	Phe	Ser	Gln	Arg	Glu	Val	Met	Leu	Ile	Met
			180					185					190		
Gly	Asp	Phe	Leu	Ser	Phe	Asn	Val	Asn	Thr	Ser	Lys	Val	Glu	Ile	Asp
	195						200					205			
Tyr	Ala	Val	Thr	Arg	Ala	Ala	Ala	Met	Arg	Ala	Tyr	Leu	Asp	Lys	Glu
	210					215					220				
Gln	Gly	Trp	His	Thr	Ser	Ile	Ser	Asn	Lys	Gly	Ile	Asn	Gly	Val	Ser
	225				230					235					240
Gly	Val	Thr	Gln	Pro	Leu	Tyr	Phe	Asp	Ile	Asn	Asp	Ser	Ser	Thr	Asp
				245					250					255	
Val	Asn	Tyr	Leu	Asn	Glu	Gln	Gly	Ile	Thr	Cys	Cys	Val	Asn	His	Asn
			260					265					270		
Gly	Phe	Arg	Phe	Trp	Gly	Leu	Arg	Thr	Thr	Ala	Glu	Asp	Pro	Leu	Phe
		275					280					285			
Lys	Phe	Glu	Val	Tyr	Thr	Arg	Thr	Ala	Gln	Ile	Leu	Lys	Asp	Thr	Ile
	290					295					300				
Ala	Gly	Ala	Phe	Asp	Trp	Ala	Val	Asp	Lys	Asp	Ile	Ser	Val	Thr	Leu
	305				310					315					320
Val	Lys	Asp	Ile	Ile	Glu	Ala	Ile	Asn	Ala	Lys	Trp	Arg	Asp	Tyr	Thr
			325						330					335	
Thr	Lys	Gly	Tyr	Leu	Ile	Gly	Gly	Lys	Ala	Trp	Leu	Asn	Lys	Glu	Leu
			340					345					350		
Asn	Ser	Ala	Thr	Asn	Leu	Lys	Asp	Ala	Lys	Leu	Leu	Ile	Ser	Tyr	Asp
		355					360					365			
Tyr	His	Pro	Val	Pro	Pro	Leu	Glu	Gln	Leu	Gly	Phe	Asn	Gln	Tyr	Ile
	370					375					380				
Ser	Asp	Glu	Tyr	Leu	Val	Asp	Phe	Ser	Asn	Arg	Leu	Ala	Ser		
	385				390					395					

<210> 51
 <211> 353
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(351)

<220>
 <223> unknown C1

<400> 51
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 1 5 10 15
 cta att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc 96
 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
 20 25 30
 tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt 144
 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45
 gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt 192
 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60
 gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240
 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65 70 75 80
 aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288
 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95
 gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110
 gtc atc tat aaa aga ta 353
 Val Ile Tyr Lys Arg
 115

<210> 52
 <211> 117
 <212> PRT
 <213> Pasteurella multocida

<400> 52
 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1 5 10 15
 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
 20 25 30
 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45
 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60

Asp	Ser	Ser	Asn	Ile	Pro	Leu	Phe	Arg	Ser	Asn	Trp	Glu	Leu	Ile	Ile	
65					70					75					80	
Asn	Asn	Ile	Tyr	Asp	Val	Val	Cys	Leu	Ser	Thr	Lys	Val	Phe	Phe	Leu	
				85					90					95		
Asp	Asp	Glu	Lys	Leu	Met	Met	Glu	Leu	Phe	Pro	Glu	Asp	Lys	Val	Arg	
			100					105					110			
Val	Ile	Tyr	Lys	Arg												
			115													

<210> 53
 <211> 509
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(507)

<220>
 <223> unknown C2

<400> 53																	
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Met	Lys	Asn	Phe	Arg	Asn	Ile	Asn	Ile	Tyr	Ser	Asp	Tyr	Gly	Lys	Val		
1				5					10					15			
gat	aag	gaa	att	ata	tta	gaa	ttc	gaa	aat	gaa	ttt	aat	ata	aag	ctt	96	
Asp	Lys	Glu	Ile	Ile	Leu	Glu	Phe	Glu	Asn	Glu	Phe	Asn	Ile	Lys	Leu		
			20					25					30				
cct	tct	tta	tac	ata	gat	tta	att	acg	gcg	cat	aat	gct	ccg	aag	agt	144	
Pro	Ser	Leu	Tyr	Ile	Asp	Leu	Ile	Thr	Ala	His	Asn	Ala	Pro	Lys	Ser		
		35				40						45					
gaa	gag	aat	tgc	ttt	gaa	tat	tac	aat	gag	cgt	aat	gag	ccc	acg	ttt	192	
Glu	Glu	Asn	Cys	Phe	Glu	Tyr	Tyr	Asn	Glu	Arg	Asn	Glu	Pro	Thr	Phe		
	50				55						60						
tct	tcc	ttt	gga	ttt	gaa	ggg	ttt	gag	aca	gag	cgg	tct	agc	gcc	tct	240	
Ser	Ser	Phe	Gly	Phe	Glu	Gly	Phe	Glu	Thr	Glu	Arg	Ser	Ser	Ala	Ser		
	65				70					75					80		
ctt	gaa	aat	ata	tat	gct	cag	tat	att	tat	gat	gat	cca	atc	tat	ggg	288	
Leu	Glu	Asn	Ile	Tyr	Ala	Gln	Tyr	Ile	Tyr	Asp	Asp	Pro	Ile	Tyr	Gly		
				85					90					95			
tat	gaa	cat	gtg	tat	tct	ttt	ggg	agt	act	ggc	gag	gga	cat	ttt	atc	336	
Tyr	Glu	His	Val	Tyr	Ser	Phe	Gly	Ser	Thr	Gly	Glu	Gly	His	Phe	Ile		
			100					105					110				
tgt	ttt	gat	tat	cgt	gat	gat	cca	aaa	ggg	gat	gaa	ccc	aaa	atc	tgt	384	
Cys	Phe	Asp	Tyr	Arg	Asp	Asp	Pro	Lys	Gly	Asp	Glu	Pro	Lys	Ile	Cys		
		115					120					125					
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Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
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Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
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Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
85 90 95

Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
100 105 110

Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
115 120 125

Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
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Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val	20	25	30	
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Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu	35	40	45	
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Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg	50	55	60	
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Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp	85	90	95	
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Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu	100	105	110	
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Lys Ala Arg Leu Ala Gln Gly Met Asp Gln Ala Ala Leu Ala Leu Val
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cca atc act att gat aaa cct ttt cat tat tca tgt gag gag tta gat 3129

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Thr Leu Thr Thr Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu				
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Gln Leu Gly Lys Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg				
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Ile Ala Phe Val Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala				
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 ctcaacttgt gttgctgcaa cgactttacc gttacgctca ctcactttaa tcgagatcac 5388
 gcctttggtg ttacgtgatt tagttgggta ttccgctaatt tcagtacgtt taccataacc 5448
 gttttgtgtg gcgggttaaaa tggcgccttc attttttTga ataacaagtg acacgacttt 5508
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 tgctgcacgc cccatggcac gcacagcatt ttactaaag cgaactacac gtccttTgtgc 5688
 ggagaagagc atgattttcat ttgaccatc ggtgatattc acaccgataa gttcgtcttc 5748
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<210> 61
 <211> 257
 <212> PRT
 <213> Pasteurella multocida

<400> 61
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 Ser Val Val Gly Cys Ser Thr His Ser Gln Gln Gly Met Thr Gln Lys
 20 25 30
 Ser Met Ser Ser Glu Thr Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser
 35 40 45
 Thr Gln Asn Tyr Ser Ala Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys
 50 55 60
 Ala Lys Glu Asp Pro Ser Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr
 65 70 75 80
 Gln Arg Gly Asp Ser Lys Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu
 85 90 95
 Asn Asp Asn Thr Lys Leu Ala Thr Gln Ala Lys Ile Leu Gln Ile Lys
 100 105 110
 Asn Leu Ile Gln Leu Asn Asn Phe Gln Glu Ala Ile Ser Val Ala Asn
 115 120 125
 Glu Leu Leu Leu Lys Ser Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg
 130 135 140
 Gly Ile Ala Tyr Ala Gln Asn Gly Asn Leu Val Asn Ala Arg Asn Asp
 145 150 155 160
 Ile Asn Lys Ala Arg Glu Phe Phe Ile Asn Asp Asn Val Ala Ile Asn
 165 170 175
 Asn Leu Ala Met Leu Asn Ile Ile Asn Gly Asp Phe Asn Asn Ala Val
 180 185 190

Ser	Leu	Leu	Leu	Pro	Gln	Tyr	Leu	Asn	Gly	Val	Lys	Asn	Ser	Arg	Leu
	195						200					205			
Ile	His	Asn	Leu	Val	Phe	Ala	Leu	Val	Lys	Asn	Gly	Asp	Leu	Asp	Tyr
	210					215					220				
Ala	Lys	Asp	Ile	Ile	Val	Lys	Glu	Arg	Leu	Asn	Thr	Ser	Pro	Asp	Asp
225					230					235					240
Leu	Ile	Asn	Ala	Leu	Lys	Lys	Thr	Thr	His	Val	Ser	Lys	Gly	Val	Thr
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Arq

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<210> 62
<211> 1788
<212> DNA
<213> Pasteurella multocida
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<220>  
<221> CDS  
<222> (1) .. (600)
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<220>
<223> unknown K

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1				5				10				15				
aaa	gat	gac	acc	agt	ttt	gtg	act	gaa	gga	aat	aac	ttt	atc	aca	gca	96
Lys	Asp	Asp	Thr	Ser	Phe	Val	Thr	Glu	Gly	Asn	Asn	Phe	Ile	Thr	Ala	
20				25				30								
aaa	gac	aac	tta	gaa	atc	acg	gca	aaa	aat	gtt	caa	att	gat	caa	gcg	144
Lys	Asp	Asn	Leu	Glu	Ile	Thr	Ala	Lys	Asn	Val	Gln	Ile	Asp	Gln	Ala	
35				40				45								
aaa	aat	att	caa	tta	aac	gcg	aat	atc	acg	atc	aat	acc	aag	tct	ggg	192
Lys	Asn	Ile	Gln	Leu	Asn	Ala	Asn	Ile	Thr	Ile	Asn	Thr	Lys	Ser	Gly	
50				55				60								
ttt	gtg	aat	tac	ggg	acc	tta	gca	agt	gct	caa	aat	tta	acg	att	aat	240
Phe	Val	Asn	Tyr	Gly	Thr	Leu	Ala	Ser	Ala	Gln	Asn	Leu	Thr	Ile	Asn	
65				70				75				80				
acc	gaa	caa	ggc	agc	att	tat	aac	ata	ggc	ggg	atc	ttg	ggg	gcg	ggg	288
Thr	Glu	Gln	Gly	Ser	Ile	Tyr	Asn	Ile	Gly	Gly	Ile	Leu	Gly	Ala	Gly	
85				90				95								
aaa	agt	ttg	aat	ctg	agc	gcg	aaa	aga	gga	gaa	aac	caa	gga	gga	tat	336
Lys	Ser	Leu	Asn	Leu	Ser	Ala	Lys	Arg	Gly	Glu	Asn	Gln	Gly	Gly	Tyr	
100				105				110								
ctt	att	aat	caa	ggg	aag	agt	cta	ctc	cat	tct	gaa	ggc	gcc	atg	aac	384
Leu	Ile	Asn	Gln	Gly	Lys	Ser	Leu	Leu	His	Ser	Glu	Gly	Ala	Met	Asn	
115				120				125								
ctc	aca	gcg	gat	cgc	acg	gtg	tac	aat	tta	ggg	aat	att	ttt	gct	aaa	432
Leu	Thr	Ala	Asp	Arg	Thr	Val	Tyr	Asn	Leu	Gly	Asn	Ile	Phe	Ala	Lys	

130	135	140	
ggt gac gcg acg atc aat gca aac gcg tta att aat gat gtt act ctc			480
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu			
145	150	155	160
aca ggt cgt ctt gag tat caa gat ctg aaa aaa gat tat acg cgt tat			528
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr			
	165	170	175
tat cgt atc aat gaa acg gca aaa cat ggt tgg cat aat aac ttc tat			576
Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr			
	180	185	190
gaa tta aac gtc gac aga gtt tct tgatttgtgc atcaattttg taaccaccgg			630
Glu Leu Asn Val Asp Arg Val Ser			
	195	200	
ttaataaaac accagcaatt tcaacgccat tcatggcaga taatgccgct gcgacgatca			690
catcaggacg atccgcggaa gtgacaagta aacttccaac gcggaaatgt tccaccatat			750
tggtcaaatt acgtgcacag aaagtgatgc cacgaatgcg acgttcattg atcgcgctt			810
catgaataat ggcagcacct aaatgtttgg ctaaataaat ggcacgagtc gcaattaatt			870
ctgcgctcca aggaatacat gccaaagattt taattgggct tttctcaaat aaatgataaa			930
tctcagatac ttgattttgt gtgtgttgga aagaatcaaa aatttctgcc aagtcagggc			990
gagtacgacc agattcatca atcggcgcat taaatttatt gatcacaaca ccaagtaa			1050
tagggttatt tttgctgcca aataatgagg ctgcggcttt gatgcgttct ttgagttctg			1110
ccggtgtttc cgtcgccggt gctgcaacaa gaatgatttc cgcatacaagt gcttgagcaa			1170
tttcatagtt aatgctattg gcataagaat gcttacgcgt agggattaaa cttccacca			1230
cgacaatttc attgtttttg gcgagttggt gatgattttc aacaattttt tctagtacca			1290
catcagattg attttgaccg atgagtgatt cagctacact taacataaat gggtcactgg			1350
tttcaatggt ggtactggtg cgaataattg atgttgtgcg atcaatcata tcttcacctg			1410
agttcggtc agaaattggt ttcataaagc cgactttcgc ccctttttgc tccagtgc			1470
gtgttaaacc taagctgaca ctggttaagc ctacaccagc actaatcggg ataaggataa			1530
ttgtacgtga cataataaac cctaatttgt tgataattta tacaaaaaga aactgccgat			1590
gaatcggcag ttaattgatc tttacgcgat gcaaaggcgc gcggtatctt gtgcaataac			1650
aagttcttca ttcggttggga tcaccatggc aacaggcgta ttgtctgctg taatcacc			1710
ttcatgacca aagcgagccg ctttgttttt atctgaatcc acttgataac cgaacagttt			1770
ttaatgggtt aaggttga			1788

<210> 63
 <211> 200
 <212> PRT
 <213> Pasteurella multocida

<400> 63
Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe
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Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
20 25 30
Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
35 40 45
Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
50 55 60
Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
65 70 75 80
Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
85 90 95
Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
100 105 110
Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn
115 120 125
Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys
130 135 140
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu
145 150 155 160
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr
165 170 175
Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr
180 185 190
Glu Leu Asn Val Asp Arg Val Ser
195 200

<210> 64
<211> 278
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (108)..(278)

<220>
<223> unknown O

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cattacccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att 116
Met Lys Ile
1
act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta 164
Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
5 10 15

gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg	212
Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu	
20 25 30 35	

gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa	260
Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu Glu	
40 45 50	

agc aaa agg gga cat agt	278
Ser Lys Arg Gly His Ser	
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<210> 65
 <211> 57
 <212> PRT
 <213> Pasteurella multocida

<400> 65	
Met. Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser	
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Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala	
20 25 30	
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly	
35 40 45	
Glu Glu Glu Ser Lys Arg Gly His Ser	
50 55	

<210> 66
 <211> 1020
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(597)

<220>
 <223> unknown P

<400> 66	
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Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala	
1 5 10 15	

gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att	96
Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile	
20 25 30	

tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat	144
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr	
35 40 45	

ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa	192
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln	
50 55 60	

ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta	240
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu	

65	70	75	80	
cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc				288
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg	85	90	95	
act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca				336
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala	100	105	110	
gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca				384
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala	115	120	125	
atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc				432
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly	130	135	140	
ggt aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa				480
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys	145	150	155	160
gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc				528
Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu	165	170	175	
gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat				576
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp	180	185	190	
ttt tca aat cgt tta gca tcg taaggggtag aaaatggctt taccacgcaa				627
Phe Ser Asn Arg Leu Ala Ser	195			
acttaaattg atgaatttaa tcatcgacgg taacaaatat ctcggcgaag tcacggaagt				687
gactcaacca aaattagcaa tgaaaatcga agaatttcgc gcgggcggta tgattggttc				747
gggtggatgtc aatctcgggc ttgaaaagct cgaagcggaa tttaaagccg gtggctacat				807
ggtcgaatta attaaaaaat tcggcgggtc aatcaacggc attccattgc gttttcttgg				867
ctcatatcag cgtgatgaca cagaagaagt cacatctgtt gagcttgtga tgcaaggctcg				927
atttactgaa attgacagcg gaaacagcaa agtgggcgat gacactgaac aaacattcaa				987
agtgccttta acgtattaca aaatcattgt tga				1020
<210> 67				
<211> 199				
<212> PRT				
<213> Pasteurella multocida				
<400> 67				
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Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile	20	25	30	
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr	35	40	45	

Phe	Asp	Ile	Asn	Asp	Ser	Ser	Thr	Asp	Val	Asn	Tyr	Leu	Asn	Glu	Gln
	50					55					60				
Gly	Ile	Thr	Cys	Cys	Val	Asn	His	Asn	Gly	Phe	Arg	Phe	Trp	Gly	Leu
65					70					75					80
Arg	Thr	Thr	Ala	Glu	Asp	Pro	Leu	Phe	Lys	Phe	Glu	Val	Tyr	Thr	Arg
				85					90					95	
Thr	Ala	Gln	Ile	Leu	Lys	Asp	Thr	Ile	Ala	Gly	Ala	Phe	Asp	Trp	Ala
			100					105					110		
Val	Asp	Lys	Asp	Ile	Ser	Val	Thr	Leu	Val	Lys	Asp	Ile	Ile	Glu	Ala
		115					120					125			
Ile	Asn	Ala	Lys	Trp	Arg	Asp	Tyr	Thr	Thr	Lys	Gly	Tyr	Leu	Ile	Gly
	130					135					140				
Gly	Lys	Ala	Trp	Leu	Asn	Lys	Glu	Leu	Asn	Ser	Ala	Thr	Asn	Leu	Lys
145					150					155					160
Asp	Ala	Lys	Leu	Leu	Ile	Ser	Tyr	Asp	Tyr	His	Pro	Val	Pro	Pro	Leu
			165						170					175	
Glu	Gln	Leu	Gly	Phe	Asn	Gln	Tyr	Ile	Ser	Asp	Glu	Tyr	Leu	Val	Asp
		180						185					190		
Phe	Ser	Asn	Arg	Leu	Ala	Ser									
		195													

<210> 68
 <211> 2584
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1042)..(2286)

<220>
 <223> xylA

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 cgcgatgggtc tttttggtct ttatttacgt gctgttttagc agtattgtgg catttaaaat 180
 cggtcgccccg ttaattcagc tcaattttgc caatgaacgc ttaaacgcca actaccgtta 240
 ttcacttata cgtctgaaag aatatgctga aagcattgct ttttatcgtg gtgaaaaaat 300
 ggaaaaacgt ctattgacca cacaatttaa tcagggtgatt gataacgttt ggcaagtaat 360
 ctaccgcacc ttgaaattat ccggttttaa cttaatcatt acgcagattt cgggtggttt 420
 tccgctgggtg attcaagtga cacgttattt tcgtcgacaa taggtgcata tgagggtggt 480
 agaatagcga tactttctgt tggaaaagta aactctttta tataaataga aatcgcttga 540
 atgattctcg ggcaaaaaat aatgtactca ttgcatct catactgata atggcgaagt 600

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aaatatcttc ttacaatatt atggtaatta tcaggtaata ccgtatagcc atagattcca 660
gttctatttt gttttgctaa ataattgatg agcatttgag gcgcaggtaa atccatatct 720
gcaacagaca ttgaaatcat atccttgccg tatttacgag taattgcca ttagcacta 780
tgacaatctg atctatcagt aaaaacatca aacaaattat ccgtcataca tgttctccaa 840
tattggattt atataaactt tagaacttga ggtagattgt tggaattgtt aaatctggta 900
tttctattac gttttttctt ttttgtgata taagccacaa taaccaataa tcttaattgt 960
taagtgaat aacgtaattg atcctcccat tgttttacta aattatgtct ctgaaactta 1020
tttgttcagg agaaatcatt t atg tcc act tac ttc gac aaa att gaa aaa 1071
                        Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys
                        1                               5              10

gta aat tat gaa ggt gta act tca tct aat ccg ttt gca tat aag cat 1119
Val Asn Tyr Glu Gly Val Thr Ser Ser Asn Pro Phe Ala Tyr Lys His
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tat gat gct aat caa gtt att tta ggt aag acg atg gct gaa cac tta 1167
Tyr Asp Ala Asn Gln Val Ile Leu Gly Lys Thr Met Ala Glu His Leu
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cgt tta gcc gtc tgt tat tgg cac act ttc tgt tgg aca ggg aat gat 1215
Arg Leu Ala Val Cys Tyr Trp His Thr Phe Cys Trp Thr Gly Asn Asp
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atg ttc ggt gtc ggt tct ttc gat cgt tgt tgg cag aag gcg agt gat 1263
Met Phe Gly Val Gly Ser Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp
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tca tta gca ggt gca aaa caa aaa gca gat atc gct ttt gaa ttt ttc 1311
Ser Leu Ala Gly Ala Lys Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe
                        75                               80              85              90

agt aaa tta ggc ata cct tat tat tgt ttt cat gat gtt gat gtt gcg 1359
Ser Lys Leu Gly Ile Pro Tyr Tyr Cys Phe His Asp Val Asp Val Ala
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cca gaa ggt cat tca ttt aaa gaa tat ttg tgc aac ttt aat aca atg 1407
Pro Glu Gly His Ser Phe Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met
                        110                               115              120

atc gat gtt tta gcg cag aaa caa gaa gaa aca ggc gtc aaa ttg ttg 1455
Ile Asp Val Leu Ala Gln Lys Gln Glu Glu Thr Gly Val Lys Leu Leu
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tgg ggg act gca aat tgt ttt aca cac cct cgt tat atg tct ggt gct 1503
Trp Gly Thr Ala Asn Cys Phe Thr His Pro Arg Tyr Met Ser Gly Ala
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gca aca aat ccg aat cca gaa att ttt gct tgg gct gct gca caa gta 1551
Ala Thr Asn Pro Asn Pro Glu Ile Phe Ala Trp Ala Ala Ala Gln Val
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Tyr	Gly	Phe	Leu	Lys	Gln	Phe	Gly	Leu	Glu	Lys	Glu	Ile	Lys	Val	Asn	
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Ile	Glu	Ala	Asn	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	
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Val	Ala	Met	Ala	Thr	Ala	Leu	Asp	Ile	Phe	Gly	Ser	Ile	Asp	Ala	Asn	
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Arg	Gly	Asp	Pro	Gln	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Asn	Ser	
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Phe	Thr	Thr	Gly	Gly	Phe	Asn	Phe	Asp	Ala	Lys	Ile	Arg	Arg	Gln	Ser	
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Thr	Asp	Pro	Tyr	Asp	Leu	Phe	His	Gly	His	Ile	Gly	Ala	Ile	Asp	Val	
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Leu	Ala	Leu	Ser	Leu	Lys	Cys	Ala	Ala	Lys	Met	Leu	Glu	Glu	Gln	Ala	
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35 40 45
Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser
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65 70 75 80
Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro
85 90 95
Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
100 105 110
Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
115 120 125
Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
130 135 140
Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
145 150 155 160
Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
165 170 175
Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
180 185 190
Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
195 200 205
Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly
210 215 220
Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys
225 230 235 240
His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln
245 250 255
Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala
260 265 270

Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Val	Ala	Met	Ala	Thr	Ala
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Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Asn	Ser	Val	Glu	Glu	Asn	Thr	Leu
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Val	Ile	Tyr	Glu	Ile	Leu	Lys	Ala	Gly	Gly	Phe	Thr	Thr	Gly	Gly	Phe
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Asn	Phe	Asp	Ala	Lys	Ile	Arg	Arg	Gln	Ser	Thr	Asp	Pro	Tyr	Asp	Leu
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Phe	His	Gly	His	Ile	Gly	Ala	Ile	Asp	Val	Leu	Ala	Leu	Ser	Leu	Lys
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Cys	Ala	Ala	Lys	Met	Leu	Glu	Glu	Gln	Ala	Leu	Gln	Lys	Val	Val	Asn
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Gln	Arg	Tyr	Ala	Gly	Trp	Thr	Ser	Ser	Leu	Gly	Gln	Leu	Val	Gln	Ile
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 cttagagcca cccaaatgaa cacgaaagtg ctcgatacct caaaagtgaa tgccgaacaa 240
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 atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt 345
 Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
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 Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala
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 Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
 35 40 45

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Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln	
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gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt ggc att gta gca	537
Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala	
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cga gcc ttt ttt tat caa ccg ttt gtg ggc aag aaa ctg atc ctc aaa	585
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys	
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Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly	
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Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln	
115 120 125	
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Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile	
130 135 140	
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Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe	
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Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala	
165 170 175	
caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc	873
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro	
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Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu	
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Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys	
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Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe	
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Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val	
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Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu	
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Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe	
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Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser	
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Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe	
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Ala Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser	
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Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro	
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Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp	
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Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn	
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Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly	
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Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met	
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Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr	
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Arg	Ala	Phe	Phe	Tyr	Gln	Pro	Phe	Val	Gly	Lys	Lys	Leu	Ile	Leu	Lys
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Leu	Gln	Gly	Leu	Gln	Ala	Ile	Pro	Val	Gln	Gln	Arg	Gln	Leu	Ala	Ala
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Gln	Leu	Asn	Leu	Arg	Gly	Trp	His	Phe	Ile	Arg	Leu	Ile	Glu	Trp	Pro
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Tyr	Leu	Arg	Gln	Gln	Leu	Leu	Pro	Ala	Phe	Thr	Leu	Ile	Phe	Met	Leu
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Asp	Val	Pro	Lys	Ala	Gly	Leu	Phe	Ala	Leu	Leu	Gln	Phe	Val	Phe	Cys
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Thr	Leu	His	Ser	Gln	Pro	Thr	Trp	Phe	Ala	Pro	Gln	Ser	Tyr	Trp	Val
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Lys	Leu	Trp	Gln	Arg	Met	Ile	Ile	Val	Cys	Ala	Thr	Val	Phe	Ile	Leu
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Phe	Thr	Leu	Trp	Leu	Gln	Pro	Gln	Leu	Trp	Lys	Ala	Leu	Gly	Tyr	Ser
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Phe	Ser	Pro	Tyr	His	Leu	Phe	Gly	Val	Val	Val	Cys	Cys	Asn	Ala	Leu
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Asn	Met	Ile	Tyr	Tyr	Glu	Lys	Leu	Cys	Gln	Ser	Leu	Asn	Leu	Arg	Gly
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gca aca tta ctt gat aag act gga att gct aga gat ctc tac aac gca 1891

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Phe	Ile	Ala	Asn	Leu	Phe	Ala	Ser	Leu	Asp	Ala	Ser	Pro	Ile	Tyr	Thr		
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atc aat ttg tgt ttt gac ata gtc agg tac agt att tgg cgt ggt ccc 2755
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Ile Gly Met Pro Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile
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Ser Tyr Leu Trp Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser
 65 70 75 80

Arg Val Thr Asp Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met
 85 90 95

Phe Val Leu Met Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp
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Leu Tyr Asn Ala Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile
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Ala Ile Gln Ser Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly

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Met Leu Arg Leu Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val 165 170 175		
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Leu Val Leu Cys Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser 225 230 235 240		
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Asp Ile Ala Ile Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile 260 265 270		
Tyr Gly Gly Ile Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val 275 280 285		
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Val Gln Glu Ser Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile 305 310 315 320		
Trp Val Gly Ile Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met 325 330 335		
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<222> (463)..(936)

<220>

<223> yhcJ

<400> 74

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Ser Cys Lys Asn Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg
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Asp Ala Cys Ala Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro
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<210> 76
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<212> DNA
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<222> (1949)..(2785)

<220>
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Ser Ala Arg Phe Gln Ile Tyr Phe Pro Glu Ala Glu Val Phe Ala Leu	
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<213> Pasteurella multocida

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Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr
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Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu
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Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu
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Glu Val Tyr Leu Ala Leu Gln Thr Asn Ser Val Asp Gly Gln Glu Asn
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Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val
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Glu	Asn	Asn	His	Pro	Ser	Phe	Pro	Ala	Arg	Ser	Cys	Val	Glu	Val	Ala
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Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val Gly Gly Cys Val	
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35 40 45
Cys Ser Ile Arg Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly
50 55 60
Arg Trp Lys Glu Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val
65 70 75 80
Gly Gly Cys Val Ala Ser Gln Glu Gly Glu His Ile Arg Thr Arg Ala
85 90 95
Pro Tyr Val Asp Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro
100 105 110
Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val
115 120 125
Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala
130 135 140
Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr
145 150 155 160
Cys Ser Phe Cys Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg
165 170 175
Pro Val Asp Asp Val Leu Phe Glu Ile Ala Gln Leu Ala Glu Gln Gly
180 185 190
Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly
195 200 205
Ala Thr His Asp Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu
210 215 220

- 163 -

Val Ala Ala Ile Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His
225 230 235 240

Pro Ile Glu Phe Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro
245 250 255

Glu Leu Val Ser Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg
260 265 270

Val Leu Ser Met Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser
275 280 285

Ile Ile Arg Lys Leu Arg Ala Val Arg Pro Glu Ile Gln Ile Ser Ser
290 295 300

Asp Phe Ile Val Gly Phe Pro Gly Glu Thr Ala Glu Asp Phe Glu Gln
305 310 315 320

Thr Met Asn Leu Ile Ala Gln Val Asn Phe Asp Met Ser Phe Ser Phe
325 330 335

Ile Tyr Ser Ala Arg Pro Gly Thr Pro Ala Ala Asp Met Pro Asp Asp
340 345 350

Val Thr Glu Glu Glu Lys Lys Gln Arg Leu Tyr Val Leu Gln Gln Arg
355 360 365

Ile Asn Asn Gln Ala Ala Gln Phe Ser Arg Ala Met Leu Gly Thr Glu
370 375 380

Gln Arg Val Leu Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu
385 390 395 400

Thr Gly Arg Thr Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro
405 410 415

Asp Met Ile Gly Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr
420 425 430

Asn Ser Leu Arg Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu
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<213> Pasteurella multocida

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Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro Pro Phe Ala
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ctt gag aat gag aaa gcg ttt tct gct gcg tgc att cgt tgt ggt cag 607
Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg Cys Gly Gln
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Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala Ser Leu Ile
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tca ccg atg gaa gca ggt aca ccg tat ttc att gcg cgc gat aag ccc 703
Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg Asp Lys Pro
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tgt gaa atg tgt gtg gat att cct tgt gca aaa gcc tgc cca acc ggt 751
Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys Pro Thr Gly
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gca ttg gat aat caa gca aca gaa atc gat gat gcg cgt atg ggg tta 799
Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg Met Gly Leu
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gct gtc ctg cta gat cat gaa act tgt ctg aac tgg caa ggt tta cgc 847
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tgt gat gtg tgt tat cgc gtc tgt ccg ctg att aat aaa gcg att acg 895
Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys Ala Ile Thr
                150                155                160

tta gtg atg cat cgt aat gag cgt acg ggt aag cac gcc gtc ttt atc 943
Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala Val Phe Ile
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cca aca gtg cat tcc gaa gcc tgt aca gga tgt ggc aaa tgt gaa gaa 991
Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys Cys Glu Glu
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gct tgc gtt cta gaa gaa gcg gca atc aaa gtg tta ccg atg gca tta 1039

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Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp Glu Glu Lys				
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gaa aaa gcc ggg cat tcc ctt gcg cca gaa ggc att att tct ctc ccg	1135			
Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile Ser Leu Pro				
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act cgg tta ccg gag agc ttg taatggcaaa ttcaccaaaa tatgcgggta	1186			
Thr Arg Leu Pro Glu Ser Leu				
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 <212> PRT
 <213> Pasteurella multocida

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 Pro Phe Ala Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg
 50 55 60
 Cys Gly Gln Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala
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 Ser Leu Ile Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg
 85 90 95
 Asp Lys Pro Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys
 100 105 110
 Pro Thr Gly Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg
 115 120 125
 Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln
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 Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys
 145 150 155 160
 Ala Ile Thr Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala
 165 170 175
 Val Phe Ile Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys
 180 185 190
 Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
 195 200 205
 Met Ala Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp
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245

250

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Leu Ser Tyr Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr
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atg agt att cat ttt gat aca tta aat aat aac gct gtt cgc ttt ctc      2545
Met Ser Ile His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu
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tca ggg ggc agc gtt ttt att tta gcc tgt ttt ttt tat tat cgc gct      2593
Ser Gly Gly Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala
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Glu Leu Thr Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro
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agt tca agt tta ggt ttc tta ata ttg aaa act gta cca tct ttt tca      2689
Ser Ser Ser Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser
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tac gtt aca atc tca aca ctt aat cgc gtt tgaccttcg atttttgata      2739
Tyr Val Thr Ile Ser Thr Leu Asn Arg Val
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gtcagaataa gtactgccgg tatatcgtct taatctaaga ttaagcttgc cacttttgtt 2859

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- 170 -

cgataaagcg tcaaacgaaa gcacgacttt accgtccttg acttccacct gatcttcaat 2919
gagcacttga cttagtgcga ccaatcgacc gttggcagtc agtgtcgcaa tgccgtgac 2979
cgtatcaagc gttacaccgc tattttttcc ccagttttta ttgagctttt cactatgttt 3039
cagtaagttt ctgccaccaa tctgcaactg attaaactta gcttcaagcg tttcactctt 3099
gactgcaagc gacttgtttt cattgctaac cgtctgctca agtgctgtga ttttggatgt 3159
taaatactaac ttagttgcat tgacttcac agtccattct gactttaact cttttctcgc 3219
aagtgcgcgc acttcatctt tgctagcttt cgtttctttt aagtcagaaa tgccactagt 3279
attttgcgcc actttagaat cgagcgtttc tagttttgta gagaaagatt tgtctttttc 3339
gctagccgtt ttttgaatta gctgtatttc actttcgtc aatccaactc tagcagttag 3399
actgtctagc ttgtcagcag tagatttatt cacagtcgct tgtgattgct tgtgttgaat 3459
aatatccgcg cttacttccg agatagccac gtcga 3494

<210> 85
<211> 103
<212> PRT
<213> *Pasteurella multocida*

<400> 85
Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys Leu Ser Tyr
1 5 10 15
Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr Met Ser Ile
20 25 30
His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu Ser Gly Gly
35 40 45
Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala Glu Leu Thr
50 55 60
Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro Ser Ser Ser
65 70 75 80
Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser Tyr Val Thr
85 90 95
Ile Ser Thr Leu Asn Arg Val
100

<210> 86
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 86
aggccggtac cggccgcct

<210> 87
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 87
cggccggtac cggcctagg 19

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 88
catggtaccc attctaac 18

<210> 89
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 89
ctaggtacct acaacctc 18

<210> 90
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: transposon
insert

<220>
<223> Nucleotides designated "n" are A, T, G or C.

<400> 90
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nknknknknk nknknknknk nknknknknk nknkaagctt ggtagaatg ggtaccatg 119

<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 91

tacctacaac ctcaagct 18

<210> 92
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 92
taccattct aaccaagc 18

<210> 93
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 93
tacctacaac ctcaagctt 19

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 94
taccattct aaccaagctt 20

<210> 95
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 95
ggcagagcat tacgctgac 19

<210> 96
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 96
gtaccggcca ggcggccacg cgtattc 27

<210> 97
<211> 531
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> atpG

<400> 97
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cgtgagatct caagtaacgg gattaggcga taatccggaa atggaacgta tcgtgggcg 120
agttaatgaa atgattaatg cgttccgaaa cggagaagtg gatgcgggtt acgtcgctta 180
caaccgtttt gaaaatacga tgtcacaaaa acctgttatc gcacagttac ttccggttacc 240
taaactagat gacgatgaat tagatacgaa aggttcatgg gattatattt atgaaccgaa 300
tccacaagtt ttattggata gtttacttgt tcgttattta gaaactcagg tataccaagc 360
agttgtagat aacctagctt ctgaacaagc cgctcgaatg gtagcgatga aagccgcaac 420
agataatgcg ggtacattaa tcgatgaatt acaattagtg tataacaaag ctcgccaagc 480
aagcattaca aatgaattaa acgaaattgt tgcgggtgcc gcagcaattt a 531

<210> 98
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 98
tctccattcc cttgctgagg cacc 25

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 99
ggattacagc cggatccggg 20

<210> 100
<211> 1034
<212> DNA
<213> *Pasteurella multocida*

<220>
<223> cap5E

<220>
<221> CDS
<222> (1)..(1032)

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1 5 10 15

ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att 96
Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile
20 25 30

cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa 144
Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys
35 40 45

tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac 192
Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr
50 55 60

gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct 240
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala
65 70 75 80

gcc gca tta aag caa gtg cct tca tgc gag ttt tat ccg tta gag gca 288
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala
85 90 95

gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc 336
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile
100 105 110

caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg 384
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val
115 120 125

tac cca att aat gcg atg ggc att tct aaa gca atg atg gaa aaa gtc 432
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val
130 135 140

atc atc gca aaa tcg cgt aac cta gaa ggc aca cca acg aca atc tgt 480
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys
145 150 155 160

tgt act cgc tat ggc aat gtc atg gca tcg cgt ggt tcg gtt atc cca 528
Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
165 170 175

tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat 576
Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
180 185 190

cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta 624
Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
195 200 205

gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa 672
Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
210 215 220

aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa 720
Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
225 230 235 240

tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat 768
Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His

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245										250					255					
gga	gag	aaa	gca	ttc	gaa	gct	tta	tta	agc	cgt	gaa	gaa	atg	gtt	cat	816				
Gly	Glu	Lys	Ala	Phe	Glu	Ala	Leu	Leu	Ser	Arg	Glu	Glu	Met	Val	His					
			260					265					270							
gca	att	aat	gaa	ggt	aat	tat	tat	cgc	atc	cca	gcc	gat	caa	cgc	agt	864				
Ala	Ile	Asn	Glu	Gly	Asn	Tyr	Tyr	Arg	Ile	Pro	Ala	Asp	Gln	Arg	Ser					
		275					280					285								
tta	aat	tac	agt	aaa	tat	gtc	gaa	aaa	ggg	gaa	cca	aaa	att	acc	gaa	912				
Leu	Asn	Tyr	Ser	Lys	Tyr	Val	Glu	Lys	Gly	Glu	Pro	Lys	Ile	Thr	Glu					
	290					295					300									
gtc	acc	gac	tac	aac	tca	cat	aat	act	gag	cgt	ttg	act	gtc	aag	gaa	960				
Val	Thr	Asp	Tyr	Asn	Ser	His	Asn	Thr	Glu	Arg	Leu	Thr	Val	Lys	Glu					
305					310				315						320					
atg	aag	cag	tta	ctg	ctt	aaa	ctt	gaa	ttc	ata	cag	aaa	atg	att	gag	1008				
Met	Lys	Gln	Leu	Leu	Leu	Lys	Leu	Glu	Phe	Ile	Gln	Lys	Met	Ile	Glu					
			325					330						335						
ggt	gaa	tac	atc	tca	ccg	gag	gta	ta								1034				
Gly	Glu	Tyr	Ile	Ser	Pro	Glu	Val													
			340																	

<210> 101

<211> 344

<212> PRT

<213> Pasteurella multocida

<400> 101

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			20					25					30		
Arg	Val	Phe	Ser	Arg	Asp	Glu	Lys	Lys	Gln	Asp	Asp	Met	Arg	Lys	Lys
		35				40						45			
Tyr	Asn	Asp	Ala	Lys	Leu	Lys	Phe	Tyr	Ile	Gly	Asp	Val	Arg	Asp	Tyr
	50				55					60					
Asp	Ser	Ile	Leu	Asn	Ala	Ser	Arg	Gly	Val	Asp	Tyr	Ile	Tyr	His	Ala
65				70				75						80	
Ala	Ala	Leu	Lys	Gln	Val	Pro	Ser	Cys	Glu	Phe	Tyr	Pro	Leu	Glu	Ala
			85					90					95		
Val	Lys	Thr	Asn	Ile	Leu	Gly	Thr	Ala	Asn	Val	Leu	Glu	Ala	Ala	Ile
			100					105					110		
Gln	Asn	Gln	Ile	Lys	Arg	Val	Val	Cys	Leu	Ser	Thr	Asp	Lys	Ala	Val
	115					120						125			
Tyr	Pro	Ile	Asn	Ala	Met	Gly	Ile	Ser	Lys	Ala	Met	Met	Glu	Lys	Val
	130					135					140				
Ile	Ile	Ala	Lys	Ser	Arg	Asn	Leu	Glu	Gly	Thr	Pro	Thr	Thr	Ile	Cys
145					150					155					160

Cys	Thr	Arg	Tyr	Gly	Asn	Val	Met	Ala	Ser	Arg	Gly	Ser	Val	Ile	Pro	
				165					170					175		
Leu	Phe	Val	Asp	Gln	Ile	Arg	Gln	Gly	Lys	Pro	Phe	Thr	Ile	Thr	Asp	
			180					185					190			
Pro	Glu	Met	Thr	Arg	Phe	Met	Met	Thr	Leu	Glu	Asp	Ala	Val	Asp	Leu	
		195					200					205				
Val	Leu	Tyr	Ala	Phe	Lys	Asn	Gly	Gln	Asn	Gly	Asp	Val	Phe	Val	Gln	
	210					215					220					
Lys	Ala	Pro	Ala	Ala	Thr	Ile	Gly	Thr	Leu	Ala	Lys	Ala	Ile	Thr	Glu	
225					230					235					240	
Leu	Leu	Ser	Val	Pro	Asn	His	Pro	Ile	Ser	Ile	Ile	Gly	Thr	Arg	His	
				245					250					255		
Gly	Glu	Lys	Ala	Phe	Glu	Ala	Leu	Leu	Ser	Arg	Glu	Glu	Met	Val	His	
			260					265					270			
Ala	Ile	Asn	Glu	Gly	Asn	Tyr	Tyr	Arg	Ile	Pro	Ala	Asp	Gln	Arg	Ser	
	275						280					285				
Leu	Asn	Tyr	Ser	Lys	Tyr	Val	Glu	Lys	Gly	Glu	Pro	Lys	Ile	Thr	Glu	
	290					295					300					
Val	Thr	Asp	Tyr	Asn	Ser	His	Asn	Thr	Glu	Arg	Leu	Thr	Val	Lys	Glu	
305					310					315					320	
Met	Lys	Gln	Leu	Leu	Leu	Lys	Leu	Glu	Phe	Ile	Gln	Lys	Met	Ile	Glu	
			325						330					335		
Gly	Glu	Tyr	Ile	Ser	Pro	Glu	Val									
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<210> 102

<211> 4931

<212> DNA

<213> Pasteurella multocida

<220>

<223> fhaB2

<220>

<221> CDS

<222> (1)..(4929)

<220>

<223> Nucleotide at position 4894 is A, T, G, or C. The corresponding amino acid is unknown.

<400> 102

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Met	Asn	Lys	Asn	Arg	Tyr	Lys	Leu	Ile	Phe	Ser	Gln	Val	Lys	Gly	Cys	
1				5					10					15		
ctc	ggt	cct	gtg	gca	gaa	tgt	att	aac	tca	gct	att	agc	aat	ggg	tca	96
Leu	Val	Pro	Val	Ala	Glu	Cys	Ile	Asn	Ser	Ala	Ile	Ser	Asn	Gly	Ser	
			20					25					30			
tct	gat	tca	aca	tcc	aca	tca	gaa	caa	ggt	gaa	gag	gaa	cct	ttc	ctt	144

Ser	Asp	Ser	Thr	Ser	Thr	Ser	Glu	Gln	Val	Glu	Glu	Glu	Pro	Phe	Leu	
		35					40					45				
cta	gaa	caa	tat	tca	ctt	tcc	tcc	gtg	tct	tta	tta	gta	aaa	agc	acg	192
Leu	Glu	Gln	Tyr	Ser	Leu	Ser	Ser	Val	Ser	Leu	Leu	Val	Lys	Ser	Thr	
	50					55					60					
ttc	aat	cct	gtt	tcg	tat	gca	atg	caa	ttg	act	tgg	aaa	cag	ctt	tct	240
Phe	Asn	Pro	Val	Ser	Tyr	Ala	Met	Gln	Leu	Thr	Trp	Lys	Gln	Leu	Ser	
65					70					75					80	
att	tta	ttt	tta	act	gtg	att	tct	gtt	cct	gtt	ttg	gct	gag	gga	aaa	288
Ile	Leu	Phe	Leu	Thr	Val	Ile	Ser	Val	Pro	Val	Leu	Ala	Glu	Gly	Lys	
				85					90					95		
ggg	gat	gaa	aga	aat	caa	tta	aca	gtg	att	gat	aat	agc	gat	cat	att	336
Gly	Asp	Glu	Arg	Asn	Gln	Leu	Thr	Val	Ile	Asp	Asn	Ser	Asp	His	Ile	
			100					105					110			
aaa	tta	gat	gca	tct	aat	ctt	gct	ggg	aat	gat	aaa	aca	aaa	atc	tat	384
Lys	Leu	Asp	Ala	Ser	Asn	Leu	Ala	Gly	Asn	Asp	Lys	Thr	Lys	Ile	Tyr	
		115					120					125				
caa	gca	gaa	aat	aaa	gtt	ctg	gtt	att	gat	att	gct	aaa	cca	aat	ggg	432
Gln	Ala	Glu	Asn	Lys	Val	Leu	Val	Ile	Asp	Ile	Ala	Lys	Pro	Asn	Gly	
	130					135					140					
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Lys	Gly	Ile	Ser	Asp	Asn	Arg	Phe	Glu	Lys	Phe	Asn	Ile	Pro	Asn	Ser	
145					150					155					160	
gcg	gtg	ttt	aat	aat	aat	ggg	act	gaa	gcg	cag	gca	aga	tca	aca	tta	528
Ala	Val	Phe	Asn	Asn	Asn	Gly	Thr	Glu	Ala	Gln	Ala	Arg	Ser	Thr	Leu	
				165					170					175		
att	ggt	tac	att	ccg	caa	aat	caa	aat	tta	agg	gga	ggg	aaa	gaa	gct	576
Ile	Gly	Tyr	Ile	Pro	Gln	Asn	Gln	Asn	Leu	Arg	Gly	Gly	Lys	Glu	Ala	
			180					185					190			
gat	gtt	ata	tta	aat	caa	gtg	aca	ggg	cct	caa	gaa	agt	aaa	att	gtt	624
Asp	Val	Ile	Leu	Asn	Gln	Val	Thr	Gly	Pro	Gln	Glu	Ser	Lys	Ile	Val	
		195					200					205				
ggc	gcg	ctt	gaa	gta	tta	ggg	aaa	aaa	gct	gat	atc	gtc	att	gca	aac	672
Gly	Ala	Leu	Glu	Val	Leu	Gly	Lys	Lys	Ala	Asp	Ile	Val	Ile	Ala	Asn	
	210					215					220					
caa	aat	ggg	att	acc	tta	aat	ggg	gta	aga	aca	ata	aat	tca	gat	cgt	720
Gln	Asn	Gly	Ile	Thr	Leu	Asn	Gly	Val	Arg	Thr	Ile	Asn	Ser	Asp	Arg	
225					230					235					240	
ttt	gtt	gcc	act	acg	agt	gag	ctt	ata	gat	ccg	aat	cag	atg	atg	tta	768
Phe	Val	Ala	Thr	Thr	Ser	Glu	Leu	Ile	Asp	Pro	Asn	Gln	Met	Met	Leu	
				245					250					255		
aag	gtt	aca	aaa	gga	aat	gtg	atc	att	gat	att	gat	ggg	ttt	tcg	aca	816
Lys	Val	Thr	Lys	Gly	Asn	Val	Ile	Ile	Asp	Ile	Asp	Gly	Phe	Ser	Thr	
			260					265					270			
gat	gga	tta	aag	tat	tta	gat	att	att	gct	aaa	aaa	att	gaa	caa	aag	864
Asp	Gly	Leu	Lys	Tyr	Leu	Asp	Ile	Ile	Ala	Lys	Lys	Ile	Glu	Gln	Lys	
		275					280					285				

caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act	912
Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr	
290 295 300	
ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa	960
Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys	
305 310 315 320	
aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga	1008
Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly	
325 330 335	
tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca	1056
Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr	
340 345 350	
gat. aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat	1104
Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn	
355 360 365	
gat att cag att gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg	1152
Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr	
370 375 380	
att cag caa aca gtg gta aaa aaa gac cga aat att cga gcc aag aaa	1200
Ile Gln Gln Thr Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys	
385 390 395 400	
aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg	1248
Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr	
405 410 415	
aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa	1296
Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys	
420 425 430	
aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt	1344
Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly	
435 440 445	
gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat	1392
Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp	
450 455 460	
gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag	1440
Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu	
465 470 475 480	
gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct	1488
Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala	
485 490 495	
gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att	1536
Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile	
500 505 510	
caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc	1584
Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg	
515 520 525	
ttt tta ggc tct ccg ttt ttc tca ata tct ccg tcg atg ctc gca agc	1632
Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser	
530 535 540	

ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa	1680
Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu	
545 550 555 560	
agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta	1728
Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu	
565 570 575	
aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac	1776
Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn	
580 585 590	
gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct	1824
Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala	
595 600 605	
aat ata acg ttg aat gtg gaa gaa aac ttt gtt aat cgt gca gga aca	1872
Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr	
610 615 620	
ctg gca act ggt aaa aca ctg aca att aat acc gaa agt ggc agt att	1920
Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile	
625 630 635 640	
tac aat ctt ggt ggg aca tta ggt gct gga aaa tca tta aaa ctg act	1968
Tyr Asn Leu Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr	
645 650 655	
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Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn	
660 665 670	
ggg tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag cgt tct	2064
Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser	
675 680 685	
gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca gtt cat	2112
Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His	
690 695 700	
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Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr	
705 710 715 720	
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Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val	
725 730 735	
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His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu	
740 745 750	
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Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser	
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Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser	
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Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe	
785 790 795 800	

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Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln	
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Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr	
820 825 830	
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Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala	
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tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc	2592
Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly	
850 855 860	
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Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser	
865 870 875 880	
gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa	2688
Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys	
885 890 895	
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Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp	
900 905 910	
gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc	2784
Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe	
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Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu	
930 935 940	
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Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys	
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Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser	
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980 985 990	
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Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu	
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Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Leu Ser Pro Ile	
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cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe 1090 1095 1100	3312
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gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys 1140 1145 1150	3456
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Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp	
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Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val	
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aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat	4464
Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn	
1475 1480 1485	
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Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu	
1490 1495 1500	
gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca aat gat	4560
Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp	
1505 1510 1515 1520	
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Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His	
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tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tcg	4656
Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser	
1540 1545 1550	
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1570 1575 1580

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Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
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<213> *Pasteurella multocida*

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35 40 45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
50 55 60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
65 70 75 80

Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
85 90 95

Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
100 105 110

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
115 120 125

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
130 135 140

Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
145 150 155 160

Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
165 170 175

Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
180 185 190

Asp	Val	Ile	Leu	Asn	Gln	Val	Thr	Gly	Pro	Gln	Glu	Ser	Lys	Ile	Val
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Gly	Ala	Leu	Glu	Val	Leu	Gly	Lys	Lys	Ala	Asp	Ile	Val	Ile	Ala	Asn
	210					215					220				
Gln	Asn	Gly	Ile	Thr	Leu	Asn	Gly	Val	Arg	Thr	Ile	Asn	Ser	Asp	Arg
225					230					235					240
Phe	Val	Ala	Thr	Thr	Ser	Glu	Leu	Ile	Asp	Pro	Asn	Gln	Met	Met	Leu
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Lys	Val	Thr	Lys	Gly	Asn	Val	Ile	Ile	Asp	Ile	Asp	Gly	Phe	Ser	Thr
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Asp	Gly	Leu	Lys	Tyr	Leu	Asp	Ile	Ile	Ala	Lys	Lys	Ile	Glu	Gln	Lys
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Gln	Ser	Ile	Thr	Ser	Gly	Asp	Asn	Ser	Glu	Ala	Lys	Thr	Asp	Val	Thr
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Leu	Ile	Ala	Gly	Ser	Ser	Glu	Tyr	Asp	Leu	Ser	Lys	His	Glu	Leu	Lys
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Lys	Thr	Ser	Gly	Glu	Asn	Val	Ser	Asn	Asp	Val	Ile	Ala	Ile	Thr	Gly
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Ser	Ser	Thr	Gly	Ala	Met	His	Gly	Lys	Asn	Ile	Lys	Leu	Ile	Val	Thr
			340					345					350		
Asp	Lys	Gly	Ala	Gly	Val	Lys	His	Asp	Gly	Ile	Ile	Leu	Ser	Glu	Asn
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	370					375					380				
Ile	Gln	Gln	Thr	Val	Val	Lys	Lys	Asp	Arg	Asn	Ile	Arg	Ala	Lys	Lys
385					390					395					400
Lys	Ile	Glu	Val	Lys	Asn	Ala	Asn	Arg	Val	Phe	Val	Gly	Ser	Gln	Thr
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Asn	Ala	Glu	Ile	Arg	Ser	Thr	Thr	Gln	Ala	Lys	Ile	Val	Ala	Lys	Gly
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Ala	Leu	Ser	Ile	Glu	Gln	Asn	Ala	Lys	Leu	Val	Ala	Lys	Lys	Ile	Asp
	450					455					460				
Val	Ala	Thr	Glu	Thr	Leu	Thr	Asn	Ala	Gly	Arg	Ile	Tyr	Gly	Arg	Glu
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Val	Lys	Leu	Asp	Thr	Asn	Asn	Leu	Ile	Asn	Asp	Lys	Glu	Ile	Tyr	Ala
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Glu	Arg	Lys	Leu	Ser	Ile	Leu	Thr	Lys	Gly	Lys	Asp	Leu	Glu	Ile	Ile
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Gln	Asp	Arg	Tyr	Leu	Ser	Pro	Leu	Met	Arg	Val	Lys	Ser	Ser	Val	Arg
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Leu	Ser	Ala	Gln	Phe	Lys	Pro	Gly	Phe	Val	Asn	Lys	Gly	Leu	Ile	Glu
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Ser	Ala	Gly	Ser	Ala	Glu	Leu	Thr	Phe	Lys	Glu	Lys	Thr	Ser	Phe	Leu
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Thr	Glu	Gly	Asn	Asn	Phe	Ile	Arg	Ala	Lys	Asp	Ala	Leu	Thr	Ile	Asn
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Ala	Gln	Asn	Ile	Glu	Ile	Asp	Lys	Asn	Gln	Asp	Ile	Gln	Leu	Gly	Ala
		595					600					605			
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610						615					620				
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Tyr	Asn	Leu	Gly	Gly	Thr	Leu	Gly	Ala	Gly	Lys	Ser	Leu	Lys	Leu	Thr
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Ala	Lys	Ser	Thr	Glu	Glu	Gly	Met	Gly	Asn	Ile	Val	Asn	Gln	Glu	Asn
			660					665					670		
Gly	Leu	Phe	His	Thr	Leu	Gly	Asn	Met	Met	Leu	Glu	Ala	Glu	Arg	Ser
		675					680					685			
Val	Tyr	Asn	Ile	Gly	Asp	Ile	Tyr	Ala	Ser	Lys	Lys	Leu	Thr	Val	His
690						695					700				
Thr	His	Asn	Leu	Ile	Asn	Asp	Val	Arg	Leu	Ser	Gly	Asn	Val	Ser	Tyr
705					710					715					720
Lys	Pro	Ile	Gly	Ser	Ser	Arg	Asp	Tyr	Asp	Ile	Ser	Arg	Val	Ala	Val
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His	Gly	Trp	His	Asn	Asn	Val	Tyr	Lys	Leu	Asn	Leu	Asn	Leu	Gln	Glu
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Lys	Pro	Gln	Leu	Ile	Asn	His	Gly	Leu	Ile	Asn	Val	Lys	Gly	Thr	Phe
785					790					795					800
Asn	Ala	Glu	Ala	Asp	Gln	Val	Val	Asn	Gln	Met	Lys	Ala	Phe	Asn	Gln
				805					810					815	
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Tyr	Gln	Pro	Leu	Thr	Arg	Tyr	Ile	Trp	Thr	Pro	Leu	Ser	Gly	Asn	Ala
		835					840					845			
Ser	Arg	Glu	Phe	Asn	Asn	Leu	Glu	Ser	Phe	Leu	Asp	Ala	Leu	Phe	Gly
850						855					860				

Ser	Thr	Thr	Ile	Leu	Lys	Ser	Ser	Phe	Tyr	Ser	Thr	Glu	Asn	Phe	Ser	865	870	875	880
Ala	Tyr	Gln	Leu	Leu	Ser	His	Ile	Gln	His	Ser	Pro	Met	Tyr	Gln	Lys	885	890		895
Ala	Met	Ala	Gln	Val	Phe	Gly	Ala	Glu	Trp	His	Ser	Lys	Ser	Tyr	Asp	900	905		910
Glu	Met	Arg	Asn	Lys	Trp	Lys	Ser	Phe	Lys	Glu	Asn	Pro	Thr	Asp	Phe	915	920		925
Ile	Tyr	Tyr	Pro	Ser	Glu	Lys	Ala	Lys	Ile	Leu	Ala	Gly	Lys	Leu	Glu	930	935		940
Gly	Lys	Leu	Thr	Thr	Leu	Gln	Asn	Gly	Glu	Tyr	Ala	Glu	Arg	Gly	Lys	945	950		955
Phe	Asp	Glu	Ser	Ile	Gln	Ile	Gly	Lys	His	Gln	Leu	Ser	Leu	Pro	Ser	965	970		975
Val	Glu	Leu	Lys	Ala	Glu	Phe	Ser	Asp	Lys	Glu	Arg	Leu	Glu	Glu	Asp	980	985		990
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His	Ser	Asn	Ser	Ser	Asp	Asp	Val	Leu	Ser	Met	Asn	Asp	Asp	Glu	Ser	1045	1050		1055
Asp	Thr	Asp	Asp	Ser	Lys	Trp	Ser	Met	Gly	Asn	Asp	Glu	Lys	Glu	Met	1060	1065		1070
Pro	Asp	Asp	Lys	Leu	Gly	Ile	Ser	Arg	Asp	Asp	Arg	Gly	Asn	Lys	Pro	1075	1080		1085
Pro	Arg	Thr	Asp	Pro	Thr	Val	Asp	Tyr	Leu	Asn	Pro	Asp	Glu	Phe	Phe	1090	1095		1100
Glu	Asn	Gly	Tyr	Leu	Leu	Asn	Glu	Leu	Leu	Gln	Glu	Leu	Gly	Glu	Glu	1105	1110		1115
Pro	Leu	Leu	Lys	Glu	Gly	Glu	Asp	His	Phe	Lys	Arg	Ser	Thr	Asn	Leu	1125	1130		1135
Val	Arg	Leu	Gly	Glu	Arg	Asp	Arg	Gln	Asn	Arg	Glu	Lys	Arg	Glu	Lys	1140	1145		1150
Glu	Gly	Tyr	Phe	Asp	Leu	Pro	Gly	Thr	Leu	Asp	Met	Lys	Leu	Gln	Glu	1155	1160		1165
Leu	Phe	Glu	Lys	Arg	Lys	Gln	Lys	His	Glu	Ala	Glu	Gln	Lys	Ala	Arg	1170	1175		1180
Ile	Glu	Lys	Ala	Leu	Leu	Gln	Lys	Ser	Glu	Gln	Gln	Glu	Lys	Arg	Val	1185	1190		1195
																			1200

Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
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Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
1395 1400 1405

Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
1410 1415 1420

Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
1425 1430 1435 1440

Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
1445 1450 1455

Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
1460 1465 1470

Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
1475 1480 1485

Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu
1490 1495 1500

Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp
1505 1510 1515 1520

Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
1525 1530 1535

Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser
1540 1545 1550

Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
1555 1560 1565

Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
1570 1575 1580

Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
1585 1590 1595 1600

Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
1605 1610 1615

Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
1620 1625 1630

Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
1635 1640

<210> 104
<211> 2009
<212> DNA
<213> Pasteurella multocida

<220>
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<222> (1)..(2007)

<400> 104
atc cgt ggc gtt gat aaa gat cgt gtc gct gtt att gtt gat gga ata 48
Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
1 5 10 15

cgc cag gct gaa tcg act ata tct act tcc gca cgt tat tcg act gaa 96
Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
20 25 30

cgt cat aat ggt aat att aat aat att gaa tac gaa aat gtt agt tcg 144
Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
35 40 45

ttg aaa gtt caa aaa ggg gca gct tct gta atg tat ggt agc ggt gcg 192
Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
50 55 60

tta ggt gga acc gtg gag ttt acc aca aaa gat att gag gac ttt gtc 240
Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
65 70 75 80

gaa cct ggt cgc cat ttg ggc ttt ttg tct aaa acc ggc tat act tca 288
Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
85 90 95

aaa aac aga gaa tat cgt caa gtc atc gga gtt gga ggg aaa ggg gaa 336
Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
100 105 110

cac His	ttt Phe	ttt Phe 115	ggt Gly	ttt Phe	gta Val	caa Gln	tta Leu 120	acc Thr	aaa Lys	cgt Arg	tgg Trp	ggg Gly 125	cat His	gaa Glu	aca Thr	384
atc Ile	aac Asn 130	aac Asn	ggc Gly	aaa Lys	ggt Gly	aca Thr 135	gac Asp	att Ile	ctc Leu	ggc Gly	gaa Glu 140	cat His	cga Arg	ggt Gly	aaa Lys	432
ccc Pro 145	aat Asn	ccg Pro	ctc Leu	aac Asn	tac Tyr 150	tat Tyr	act Thr	aca Thr	tca Ser	tgg Trp 155	tta Leu	acg Thr	aaa Lys	gtc Val	ggt Gly 160	480
tac Tyr	gat Asp	att Ile	aat Asn	aac Asn 165	act Thr	cat His	cgt Arg	ttt Phe 170	aca Thr	ctg Leu	ttt Phe	tta Leu	gaa Glu	gat Asp 175	cgc Arg	528
cgt Arg	gaa Glu	aag Lys	aag Lys 180	ctt Leu	acc Thr	gaa Glu	gaa Glu	aaa Lys 185	aca Thr	tta Leu	ggg Gly	ctt Leu	agt Ser 190	gat Asp	gca Ala	576
gtg Val	cgt Arg	ttt Phe 195	gct Ala	aat Asn	gat Asp	caa Gln	acc Thr 200	cct Pro	tat Tyr	ctc Leu	cgt Arg	tat Tyr 205	ggt Gly	att Ile	gaa Glu	624
tat Tyr	cga Arg 210	tat Tyr	aac Asn	ggc Gly	ttg Leu	tct Ser 215	tgg Trp	ttg Leu	gaa Glu	acg Thr	gta Val 220	aag Lys	ctt Leu	ttt Phe	ttg Leu	672
gca Ala 225	aag Lys	cag Gln	aaa Lys	atc Ile	gaa Glu 230	caa Gln	cgt Arg	tct Ser	gct Ala	ctc Leu 235	caa Gln	gag Glu	ttt Phe	gat Asp	att Ile 240	720
aat Asn	aat Asn	agg Arg	aat Asn	aaa Lys 245	ttg Leu	gat Asp	tcg Ser	act Thr	atg Met 250	tcg Ser	ttt Phe	gta Val	tat Tyr	tta Leu 255	caa Gln	768
aga Arg	cag Gln	aat Asn	ata Ile 260	gct Ala	cgg Arg	gga Gly	gaa Glu	ttt Phe 265	tca Ser	acg Thr	agt Ser	cct Pro	tta Leu 270	tat Tyr	tgg Trp	816
ggg Gly	ccg Pro	agt Ser 275	cgc Arg	cat His	cgt Arg	tta Leu	tct Ser 280	gcg Ala	aaa Lys	ttc Phe	gaa Glu	ttt Phe 285	cgt Arg	gat Asp	aag Lys	864
ttt Phe 290	tta Leu	gaa Glu	aat Asn	atg Met	aat Asn	aag Lys 295	cat His	ttt Phe	acg Thr	ttt Phe	cgg Arg 300	ccg Pro	tgg Trp	caa Gln	atc Ile	912
aat Asn 305	aga Arg	ttc Phe	aga Arg	caa Gln	caa Gln 310	ggt Gly	cga Arg	aat Asn	aac Asn	tat Tyr 315	aca Thr	gaa Glu	gtg Val	ttt Phe	ccc Pro 320	960
gtt Val	aaa Lys	tcc Ser	cga Arg	gag Glu 325	ttt Phe	tct Ser	ttt Phe	tct Ser	ctt Leu 330	atg Met	gac Asp	gac Asp	att Ile	aag Lys 335	att Ile	1008
ggc Gly	gaa Glu	ttg Leu	cta Leu 340	cat His	ctc Leu	gga Gly	ttg Leu	ggc Gly 345	ggt Gly	cgg Arg	tgg Trp	gat Asp	cac His 350	tat Tyr	aac Asn	1056
tat Tyr	aag Lys	cca Pro 355	tta Leu	tta Leu	aat Asn	tct Ser 360	cag Gln	cat His	aat Asn	atc Ile	aac Asn	agg Arg 365	aca Thr	cag Gln	aga Arg	1104

tta cct tat cca aaa aca tca tcc aaa ttt tcg tat caa ttg agt tta	1152
Leu Pro Tyr Ser Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu	
370 375 380	
gag tat caa tta cat cca tca cat caa att gca tac cgt tta agt acc	1200
Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr	
385 390 395 400	
ggg ttt agg gtt ccc cgt gtt gaa gat ctt tat ttt gaa gac cga gga	1248
Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly	
405 410 415	
aaa agt tct tca caa ttt ctt cct aac ccc gat cta caa ccg gaa act	1296
Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr	
420 425 430	
gca ctg aat cat gaa ata agt tac cgt ttc caa aat caa tat gcc cat	1344
Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His	
435 440 445	
ttc agc gtc ggg ctt ttc cgt aca cgt tat cat aac ttt att caa gaa	1392
Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu	
450 455 460	
cgt gag atg acc tgt gat aaa att cca tat gag tat aat agg act tat	1440
Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr	
465 470 475 480	
gga tat tgc acg cat aat act tat gta atg ttt gtt aat gaa cct gaa	1488
Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu	
485 490 495	
gcc gtg att aaa ggg gtt gaa gta agc ggt gct tta aat ggg tcg gca	1536
Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala	
500 505 510	
ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc	1584
Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser	
515 520 525	
aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg	1632
Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp	
530 535 540	
aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt	1680
Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser	
545 550 555 560	
ttg agc ggg cgt tat agt gcg gct aaa aaa gcc aaa gat gcg ata gaa	1728
Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu	
565 570 575	
acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta	1776
Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu	
580 585 590	
agt cca tcc tac ttt gtt gtt gat ttt acg ggg caa gtt aac ctc agt	1824
Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser	
595 600 605	
aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat	1872
Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp	
610 615 620	

tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act 1920
Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
625 630 635 640

tcc cgt tct gtc cgt gct aac agc cca ggc att aat cgg ttt acc gca 1968
Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
645 650 655

cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta 2009
Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
660 665

<210> 105

<211> 669

<212> PRT

<213> Pasteurella multocida

<400> 105

Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
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Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
20 25 30

Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
35 40 45

Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
50 55 60

Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
65 70 75 80

Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
85 90 95

Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
100 105 110

His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
115 120 125

Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
130 135 140

Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
145 150 155 160

Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
165 170 175

Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
180 185 190

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
195 200 205

Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
210 215 220

Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
225 230 235 240

Asn	Asn	Arg	Asn	Lys	Leu	Asp	Ser	Thr	Met	Ser	Phe	Val	Tyr	Leu	Gln
				245					250					255	
Arg	Gln	Asn	Ile	Ala	Arg	Gly	Glu	Phe	Ser	Thr	Ser	Pro	Leu	Tyr	Trp
			260					265					270		
Gly	Pro	Ser	Arg	His	Arg	Leu	Ser	Ala	Lys	Phe	Glu	Phe	Arg	Asp	Lys
		275					280					285			
Phe	Leu	Glu	Asn	Met	Asn	Lys	His	Phe	Thr	Phe	Arg	Pro	Trp	Gln	Ile
	290					295					300				
Asn	Arg	Phe	Arg	Gln	Gln	Gly	Arg	Asn	Asn	Tyr	Thr	Glu	Val	Phe	Pro
305					310					315					320
Val	Lys	Ser	Arg	Glu	Phe	Ser	Phe	Ser	Leu	Met	Asp	Asp	Ile	Lys	Ile
				325					330					335	
Gly	Glu	Leu	Leu	His	Leu	Gly	Leu	Gly	Gly	Arg	Trp	Asp	His	Tyr	Asn
			340					345					350		
Tyr	Lys	Pro	Leu	Leu	Asn	Ser	Gln	His	Asn	Ile	Asn	Arg	Thr	Gln	Arg
		355					360					365			
Leu	Pro	Tyr	Pro	Lys	Thr	Ser	Ser	Lys	Phe	Ser	Tyr	Gln	Leu	Ser	Leu
	370					375					380				
Glu	Tyr	Gln	Leu	His	Pro	Ser	His	Gln	Ile	Ala	Tyr	Arg	Leu	Ser	Thr
385					390					395					400
Gly	Phe	Arg	Val	Pro	Arg	Val	Glu	Asp	Leu	Tyr	Phe	Glu	Asp	Arg	Gly
				405					410					415	
Lys	Ser	Ser	Ser	Gln	Phe	Leu	Pro	Asn	Pro	Asp	Leu	Gln	Pro	Glu	Thr
			420					425					430		
Ala	Leu	Asn	His	Glu	Ile	Ser	Tyr	Arg	Phe	Gln	Asn	Gln	Tyr	Ala	His
		435					440					445			
Phe	Ser	Val	Gly	Leu	Phe	Arg	Thr	Arg	Tyr	His	Asn	Phe	Ile	Gln	Glu
	450					455					460				
Arg	Glu	Met	Thr	Cys	Asp	Lys	Ile	Pro	Tyr	Glu	Tyr	Asn	Arg	Thr	Tyr
465					470					475					480
Gly	Tyr	Cys	Thr	His	Asn	Thr	Tyr	Val	Met	Phe	Val	Asn	Glu	Pro	Glu
				485					490					495	
Ala	Val	Ile	Lys	Gly	Val	Glu	Val	Ser	Gly	Ala	Leu	Asn	Gly	Ser	Ala
			500					505					510		
Phe	Gly	Leu	Ser	Asp	Gly	Leu	Thr	Phe	Arg	Leu	Lys	Gly	Ser	Tyr	Ser
		515					520					525			
Lys	Gly	Gln	Asn	His	Asp	Gly	Asp	Pro	Leu	Lys	Ser	Ile	Gln	Pro	Trp
	530					535					540				
Thr	Val	Val	Thr	Gly	Ile	Asp	Tyr	Glu	Thr	Glu	Gly	Trp	Ser	Val	Ser
545					550					555					560
Leu	Ser	Gly	Arg	Tyr	Ser	Ala	Ala	Lys	Lys	Ala	Lys	Asp	Ala	Ile	Glu
				565					570					575	

Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
580 585 590
Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
595 600 605
Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
610 615 620
Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
625 630 635 640
Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
645 650 655
Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
660 665

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<211> 908
<212> DNA
<213> Pasteurella multocida

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<221> CDS
<222> (1)..(906)

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gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96
Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
20 25 30
tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144
Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
35 40 45
gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
50 55 60
gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240
Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
65 70 75 80
gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta 288
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
85 90 95
aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta 336
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
100 105 110
gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt 384
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
115 120 125

tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att	432
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile	
130 135 140	
tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt	480
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe	
145 150 155 160	
aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac	528
Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp	
165 170 175	
ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata	576
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile	
180 185 190	
ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt	624
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe	
195 200 205	
aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga	672
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly	
210 215 220	
aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt	720
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val	
225 230 235 240	
att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa	768
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys	
245 250 255	
cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga	816
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg	
260 265 270	
ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc	864
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala	
275 280 285	
ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta	908
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr	
290 295 300	

<210> 107

<211> 302

<212> PRT

<213> Pasteurella multocida

<400> 107

Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
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Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
20 25 30

Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
35 40 45

Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
50 55 60

- 195 -

Glu	Lys	Glu	Phe	Glu	Ser	Phe	Pro	Val	Gln	Ile	Ser	Tyr	Ile	Ser	Leu
65					70					75					80
Ala	Thr	Tyr	Ala	Arg	Leu	Lys	Ala	Ala	Glu	Tyr	Leu	Pro	Asp	Asn	Leu
				85					90					95	
Asn	Lys	Ile	Ile	Tyr	Leu	Asp	Val	Asp	Val	Leu	Val	Phe	Asn	Ser	Leu
		100						105					110		
Glu	Met	Leu	Trp	Asn	Val	Asp	Val	Asn	Asn	Phe	Leu	Thr	Ala	Ala	Cys
		115					120						125		
Tyr	Asp	Ser	Phe	Ile	Glu	Asn	Glu	Lys	Ser	Glu	His	Lys	Lys	Ser	Ile
	130					135					140				
Ser	Met	Ser	Asp	Lys	Glu	Tyr	Tyr	Phe	Asn	Ala	Gly	Val	Met	Leu	Phe
145					150					155					160
Asn	Leu	Asp	Glu	Trp	Arg	Lys	Met	Asp	Val	Phe	Ser	Arg	Ala	Leu	Asp
				165					170					175	
Leu	Leu	Ala	Met	Tyr	Pro	Asn	Gln	Met	Ile	Tyr	Gln	Asp	Gln	Asp	Ile
			180					185					190		
Leu	Asn	Ile	Leu	Phe	Arg	Asn	Lys	Val	Cys	Tyr	Leu	Asp	Cys	Arg	Phe
		195					200					205			
Asn	Phe	Met	Pro	Asn	Gln	Leu	Glu	Arg	Ile	Lys	Gln	Tyr	His	Lys	Gly
	210					215					220				
Lys	Leu	Ser	Asn	Leu	His	Ser	Leu	Glu	Lys	Thr	Thr	Met	Pro	Val	Val
225					230					235					240
Ile	Ser	His	Tyr	Cys	Gly	Pro	Glu	Lys	Ala	Trp	His	Ala	Asp	Cys	Lys
				245					250					255	
His	Phe	Asn	Val	Tyr	Phe	Tyr	Gln	Lys	Ile	Leu	Ala	Glu	Ile	Thr	Arg
			260					265					270		
Gly	Thr	Asp	Lys	Glu	Arg	Val	Leu	Ser	Ile	Lys	Thr	Tyr	Leu	Lys	Ala
		275					280						285		
Leu	Ile	Arg	Arg	Ile	Arg	Tyr	Lys	Phe	Lys	Tyr	Gln	Val	Tyr		
	290					295					300				

<210> 108

<211> 2054

<212> DNA

<213> Pasteurella multocida

<220>

<223> pnp

<220>

<221> CDS

<222> (1)..(2052)

<400> 108

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1					5				10					15		

aaa gat gtg aaa gaa ggt caa gac ttc ttc cca tta act gtt aac tat	96
Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr	
20 25 30	
caa gag cgt act tat gct gca ggc cgt att cct ggt ggc ttt ttc aaa	144
Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys	
35 40 45	
cgt gaa ggt cgt cct tct gaa ggc gaa act tta att gct cgt tta att	192
Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile	
50 55 60	
gac cgt cca att cgt cct ctt ttc cca gaa ggt ttt tat aac gaa atc	240
Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile	
65 70 75 80	
caa atc gtg gcg aca gtg gtg tct gtt aat ccg caa att tgt cca gat	288
Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp	
85 90 95	
tta gtg gca atg atc ggt gca tct gcg gca ctt tct tta tca ggt gtg	336
Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val	
100 105 110	
cca ttt aat ggc cct atc ggt gcg gca cgt gtt ggt ttt att gat gat	384
Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp	
115 120 125	
caa ttt gtg tta aac cca acc atg aac gag caa aaa caa agc cgt tta	432
Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu	
130 135 140	
gac ttg gtt gtc gcg gga aca gat aaa gcg gtg tta atg gtg gaa tct	480
Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser	
145 150 155 160	
gaa gcc gat gta tta acc gaa gaa caa atg tta gct gcg gtg gtg ttt	528
Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe	
165 170 175	
ggt cat cag caa caa caa gtg gtg att gac gcg atc aaa gaa ttt acc	576
Gly His Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr	
180 185 190	
gca gaa gcc ggt aaa ccg cgt tgg gat tgg gtg gca cct gaa cca aat	624
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Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly	
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Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp	
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Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu	
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Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile	
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Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly	
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Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr	
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Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile	
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Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys	
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Glu	Ala	Asp	Val	Leu	Thr	Glu	Glu	Gln	Met	Leu	Ala	Ala	Val	Val	Phe
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Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
35 40 45

aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta 192
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Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
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Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
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tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa 336
Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
100 105 110

gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat 384
Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
115 120 125

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Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
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aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg 480
Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
145 150 155 160

cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt 528
His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
165 170 175

cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg 576
His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
180 185 190

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50 55 60
Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
65 70 75 80
Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
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Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
100 105 110
Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
115 120 125
Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
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Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
145 150 155 160
His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
165 170 175
His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
180 185 190
Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser
195 200 205
Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val
210 215 220
Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala
225 230 235 240
Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr
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Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr
260 265 270
Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg
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Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu
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Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile
 325 330 335

Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn
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Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp
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Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg
 370 375 380

Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile
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Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu
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Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val
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Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln
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Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
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Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
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Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys	
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Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln	
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Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp	
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Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val	
115 120 125	
ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg	432
Leu Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met	
130 135 140	
act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat	480
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr	
145 150 155 160	
tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa	528
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu	
165 170 175	
gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta	576
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu	
180 185 190	
ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa	624
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys	
195 200 205	
tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act	672
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr	
210 215 220	
aaa aac ggg cac tct aga gat gtg ccg ctt tcg caa aga gct gtt gcg	720
Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala	
225 230 235 240	
cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag	768
Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln	
245 250 255	
acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag	816
Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu	
260 265 270	
tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg	864
Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu	
275 280 285	

acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc 912
 Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
 290 295 300

gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat 960
 Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
 305 310 315 320

atg agt gaa gtg gca aac ttg ttg gat ta 989
 Met Ser Glu Val Ala Asn Leu Leu Asp
 325

<210> 113

<211> 329

<212> PRT

<213> Pasteurella multocida

<400> 113

Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
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Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
 20 25 30

Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys
 35 40 45

Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln
 50 55 60

Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg
 65 70 75 80

Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp
 85 90 95

Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu
 100 105 110

Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val
 115 120 125

Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met
 130 135 140

Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr
 145 150 155 160

Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu
 165 170 175

Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu
 180 185 190

Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys
 195 200 205

Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr
 210 215 220

Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala
 225 230 235 240

Leu	Ile	Leu	Lys	Met	Lys	Glu	Val	Glu	Asn	Gly	Asp	Leu	Val	Phe	Gln	
				245					250					255		
Thr	Thr	Pro	Glu	Ser	Leu	Ser	Thr	Thr	Phe	Arg	Val	Leu	Lys	Lys	Glu	
			260					265					270			
Cys	Gly	Leu	Glu	His	Leu	His	Phe	His	Asp	Thr	Arg	Arg	Glu	Ala	Leu	
		275					280					285				
Thr	Arg	Leu	Ser	Lys	Lys	Val	Asp	Val	Met	Thr	Leu	Ala	Lys	Ile	Ser	
	290					295					300					
Gly	His	Arg	Asp	Leu	Arg	Ile	Leu	Gln	Asn	Thr	Tyr	Tyr	Ala	Pro	Asn	
305					310					315					320	
Met	Ser	Glu	Val	Ala	Asn	Leu	Leu	Asp								
				325												

<210> 114
 <211> 1190
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> sopE

<220>
 <221> CDS
 <222> (1)..(1188)

<400> 114																
atg	tct	gaa	gaa	tat	cta	cat	ggg	gtc	aaa	gtc	aca	gaa	atc	aat	caa	48
Met	Ser	Glu	Glu	Tyr	Leu	His	Gly	Val	Lys	Val	Thr	Glu	Ile	Asn	Gln	
1				5					10					15		
gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc															96	
Ala	Ile	Arg	Thr	Ile	Gln	Ser	Leu	Ser	Thr	Ala	Val	Ile	Gly	Ile	Val	
			20					25					30			
tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat gaa ccc															144	
Cys	Thr	Ala	Asn	Asp	Ala	Asp	Asn	Glu	Thr	Phe	Pro	Leu	Asn	Glu	Pro	
		35				40					45					
gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa															192	
Val	Leu	Ile	Thr	Asn	Val	Ala	Ala	Ala	Ile	Gly	Lys	Ala	Gly	Lys	Gln	
	50				55					60						
ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc aat tgc															240	
Gly	Thr	Leu	Ser	Arg	Ala	Leu	Asp	Gly	Ile	Ser	Asp	Val	Val	Asn	Cys	
	65				70				75					80		
aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa															288	
Lys	Val	Ile	Val	Val	Arg	Val	Gln	Glu	Ser	Ala	Gln	Glu	Asp	Glu	Glu	
				85				90					95			
aca aaa gca agt gaa atg aac acg gca att att ggc aca atc aca gaa															336	
Thr	Lys	Ala	Ser	Glu	Met	Asn	Thr	Ala	Ile	Ile	Gly	Thr	Ile	Thr	Glu	
			100					105					110			
gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa aac aaa															384	
Glu	Gly	Gln	Tyr	Thr	Gly	Leu	Lys	Ala	Leu	Leu	Ile	Ala	Lys	Asn	Lys	
		115					120					125				

ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa	432
Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys	
130 135 140	
gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt	480
Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe	
145 150 155 160	
gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa	528
Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln	
165 170 175	
tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg ggc gat	576
Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp	
180 185 190	
ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc	624
Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala	
195 200 205	
gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa cag ggc	672
Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly	
210 215 220	
tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc ggt gtc	720
Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val	
225 230 235 240	
aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac	768
Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn	
245 250 255	
tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat ggc ttt	816
Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe	
260 265 270	
cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt	864
Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe	
275 280 285	
gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg	912
Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly	
290 295 300	
gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta gtg aaa	960
Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys	
305 310 315 320	
gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa	1008
Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys	
325 330 335	
ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt	1056
Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser	
340 345 350	
gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac	1104
Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His	
355 360 365	
cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att tct gat	1152
Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp	
370 375 380	

gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg ta
Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385 390 395

1190

<210> 115
<211> 396
<212> PRT
<213> *Pasteurella multocida*

<400> 115
Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln
1 5 10 15
Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val
20 25 30
Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro
35 40 45
Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln
50 55 60
Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys
65 70 75 80
Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu
85 90 95
Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu
100 105 110
Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys
115 120 125
Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys
130 135 140
Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe
145 150 155 160
Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln
165 170 175
Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp
180 185 190
Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala
195 200 205
Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly
210 215 220
Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val
225 230 235 240
Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn
245 250 255
Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe
260 265 270
Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe

275					280					285					
Glu	Val	Tyr	Thr	Arg	Thr	Ala	Gln	Ile	Leu	Lys	Asp	Thr	Ile	Ala	Gly
	290					295					300				
Ala	Phe	Asp	Trp	Ala	Val	Asp	Lys	Asp	Ile	Ser	Val	Thr	Leu	Val	Lys
305					310					315					320
Asp	Ile	Ile	Glu	Ala	Ile	Asn	Ala	Lys	Trp	Arg	Asp	Tyr	Thr	Thr	Lys
				325					330					335	
Gly	Tyr	Leu	Ile	Gly	Gly	Lys	Ala	Trp	Leu	Asn	Lys	Glu	Leu	Asn	Ser
			340					345					350		
Ala	Thr	Asn	Leu	Lys	Asp	Ala	Lys	Leu	Leu	Ile	Ser	Tyr	Asp	Tyr	His
		355					360					365			
Pro	Val	Pro	Pro	Leu	Glu	Gln	Leu	Gly	Phe	Asn	Gln	Tyr	Ile	Ser	Asp
	370					375					380				
Glu	Tyr	Leu	Val	Asp	Phe	Ser	Asn	Arg	Leu	Ala	Ser				
385					390					395					

<210> 116
 <211> 2204
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> unkK

<220>
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 <222> (1) .. (2202)

<400> 116																
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Met	Asn	Lys	Asn	Arg	Tyr	Lys	Leu	Ile	Phe	Ser	Lys	Thr	Lys	Gly	Cys	
1				5					10					15		
ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca															96	
Leu	Val	Pro	Val	Ala	Glu	Thr	Ile	Asn	Ser	Ala	Val	Gly	Asn	Ala	Ser	
			20					25					30			
tca aaa gac gtt tct gac acc gag ata agt gct tct caa cca gcg ctc															144	
Ser	Lys	Asp	Val	Ser	Asp	Thr	Glu	Ile	Ser	Ala	Ser	Gln	Pro	Ala	Leu	
		35					40					45				
aac tcg ccg ctt tcg acc ctt tct gta tta gtc aaa acc gca ttt aat															192	
Asn	Ser	Pro	Leu	Ser	Thr	Leu	Ser	Val	Leu	Val	Lys	Thr	Ala	Phe	Asn	
		50				55					60					
ccg gtt tca aca ttg atg tcg ttg act tgg aaa gaa tac gcc gtt tta															240	
Pro	Val	Ser	Thr	Leu	Met	Ser	Leu	Thr	Trp	Lys	Glu	Tyr	Ala	Val	Leu	
65					70					75					80	
tta tta agt gtg gtg tct ttt cct ctt atg gca caa gcc tct gat aca															288	
Leu	Leu	Ser	Val	Val	Ser	Phe	Pro	Leu	Met	Ala	Gln	Ala	Ser	Asp	Thr	
				85				90						95		
gat tca gtg gta caa aga aaa cct gaa tta act gat gtg acg aat agc															336	
Asp	Ser	Val	Val	Gln	Arg	Lys	Pro	Glu	Leu	Thr	Asp	Val	Thr	Asn	Ser	

100							105					110					
aac	agc	tat	cat	gtg	gaa	tta	gat	aga	gag	cat	cat	aaa	ggg	gag	cat	384	
Asn	Ser	Tyr	His	Val	Glu	Leu	Asp	Arg	Glu	His	His	Lys	Gly	Glu	His		
		115					120					125					
caa	aca	aaa	atc	aaa	cat	act	gag	aat	aat	gtc	atc	att	gtt	gat	att	432	
Gln	Thr	Lys	Ile	Lys	His	Thr	Glu	Asn	Asn	Val	Ile	Ile	Val	Asp	Ile		
	130					135					140						
gca	aaa	cca	aac	caa	aag	ggc	att	tca	gat	aac	cgt	ttt	aaa	cac	ttc	480	
Ala	Lys	Pro	Asn	Gln	Lys	Gly	Ile	Ser	Asp	Asn	Arg	Phe	Lys	His	Phe		
145					150					155					160		
aac	atc	cca	aat	ggg	gcg	gta	ttt	aac	aat	agc	gcc	aag	gaa	aaa	cgc	528	
Asn	Ile	Pro	Asn	Gly	Ala	Val	Phe	Asn	Asn	Ser	Ala	Lys	Glu	Lys	Arg		
				165					170					175			
tca	cag	tta	gtg	ggg	tat	ttg	cca	ggg	aac	cag	aat	tta	acg	gaa	ggg	576	
Ser	Gln	Leu	Val	Gly	Tyr	Leu	Pro	Gly	Asn	Gln	Asn	Leu	Thr	Glu	Gly		
		180						185					190				
agt	gaa	gca	aaa	gcg	atc	tta	aat	cag	gtg	act	gga	ccg	gat	gcc	agt	624	
Ser	Glu	Ala	Lys	Ala	Ile	Leu	Asn	Gln	Val	Thr	Gly	Pro	Asp	Ala	Ser		
	195						200					205					
aaa	att	gaa	ggc	gcc	ctt	gaa	att	tta	ggg	caa	aaa	gcc	gat	ttg	gtg	672	
Lys	Ile	Glu	Gly	Ala	Leu	Glu	Ile	Leu	Gly	Gln	Lys	Ala	Asp	Leu	Val		
	210					215					220						
att	gcg	aac	caa	aat	ggc	att	gtg	ctt	aat	ggg	gta	aaa	acc	att	aat	720	
Ile	Ala	Asn	Gln	Asn	Gly	Ile	Val	Leu	Asn	Gly	Val	Lys	Thr	Ile	Asn		
225					230					235					240		
gcc	aat	cgt	ttt	gtg	gca	aca	acc	agt	agt	acc	att	gat	cct	gag	caa	768	
Ala	Asn	Arg	Phe	Val	Ala	Thr	Thr	Ser	Ser	Thr	Ile	Asp	Pro	Glu	Gln		
				245					250					255			
atg	cag	tta	aat	gtc	acg	caa	ggg	aca	gtg	aca	att	ggg	gtg	gat	gga	816	
Met	Gln	Leu	Asn	Val	Thr	Gln	Gly	Thr	Val	Thr	Ile	Gly	Val	Asp	Gly		
		260					265						270				
ttt	gcc	aca	gat	ggc	tta	cct	tat	ttg	gat	atc	att	gcc	aaa	aag	att	864	
Phe	Ala	Thr	Asp	Gly	Leu	Pro	Tyr	Leu	Asp	Ile	Ile	Ala	Lys	Lys	Ile		
		275					280					285					
gaa	caa	aaa	caa	gcg	att	aca	aaa	gaa	aga	aca	gga	aat	tcc	gaa	acc	912	
Glu	Gln	Lys	Gln	Ala	Ile	Thr	Lys	Glu	Arg	Thr	Gly	Asn	Ser	Glu	Thr		
	290					295					300						
gat	atc	act	ttt	gtc	gca	ggg	aac	agt	aaa	tat	gat	tta	aag	aca	cat	960	
Asp	Ile	Thr	Phe	Val	Ala	Gly	Asn	Ser	Lys	Tyr	Asp	Leu	Lys	Thr	His		
305					310					315					320		
caa	gtg	aca	gaa	aag	cat	acc	gct	gag	gca	caa	ggg	gaa	att	gcg	att	1008	
Gln	Val	Thr	Glu	Lys	His	Thr	Ala	Glu	Ala	Gln	Gly	Glu	Ile	Ala	Ile		
				325					330					335			
agc	ggg	gcg	agt	acc	ggg	gca	atg	tac	ggg	aaa	aat	atc	aaa	tta	atc	1056	
Ser	Gly	Ala	Ser	Thr	Gly	Ala	Met	Tyr	Gly	Lys	Asn	Ile	Lys	Leu	Ile		
			340					345					350				
gta	acg	gat	aaa	ggc	gct	ggg	gta	aaa	cat	gat	ggc	att	att	tta	tct	1104	

Val	Thr	Asp	Lys	Gly	Ala	Gly	Val	Lys	His	Asp	Gly	Ile	Ile	Leu	Ser	
		355					360					365				
gag	gcg	gat	att	caa	att	gaa	acc	cat	gag	ggc	gat	gtt	gaa	tta	ggc	1152
Glu	Ala	Asp	Ile	Gln	Ile	Glu	Thr	His	Glu	Gly	Asp	Val	Glu	Leu	Gly	
	370					375					380					
aat	aca	aaa	aat	aat	cag	aat	gag	aat	tat	gcc	aaa	gct	cat	gcg	gaa	1200
Asn	Thr	Lys	Asn	Asn	Gln	Asn	Glu	Asn	Tyr	Ala	Lys	Ala	His	Ala	Glu	
385					390					395					400	
ggg	aat	ttt	acg	gtt	aaa	ggc	ggg	aag	cac	gtt	att	att	ggg	aag	gaa	1248
Gly	Asn	Phe	Thr	Val	Lys	Gly	Gly	Lys	His	Val	Ile	Ile	Gly	Lys	Glu	
				405					410					415		
gtt	aaa	gcc	aac	aaa	gcg	gtc	gat	att	caa	gca	caa	gaa	aca	aca	gta	1296
Val	Lys	Ala	Asn	Lys	Ala	Val	Asp	Ile	Gln	Ala	Gln	Glu	Thr	Thr	Val	
			420					425					430			
aga	caa	aat	gcg	aaa	tta	act	gcc	aaa	acg	agt	gcc	aaa	att	aca	gca	1344
Arg	Gln	Asn	Ala	Lys	Leu	Thr	Ala	Lys	Thr	Ser	Ala	Lys	Ile	Thr	Ala	
		435					440					445				
agt	aag	agt	gtg	aat	ctt	gaa	gat	aac	gcg	aaa	ctt	att	gct	aat	gag	1392
Ser	Lys	Ser	Val	Asn	Leu	Glu	Asp	Asn	Ala	Lys	Leu	Ile	Ala	Asn	Glu	
	450					455					460					
ctg	agc	aca	aca	acc	aat	aaa	tta	acc	aat	aaa	ggg	agc	att	tac	ggc	1440
Leu	Ser	Thr	Thr	Thr	Asn	Lys	Leu	Thr	Asn	Lys	Gly	Ser	Ile	Tyr	Gly	
465					470					475					480	
aag	aaa	gtg	acg	cta	gat	gct	gat	aat	tta	gtc	aat	agt	aaa	gaa	atc	1488
Lys	Lys	Val	Thr	Leu	Asp	Ala	Asp	Asn	Leu	Val	Asn	Ser	Lys	Glu	Ile	
				485					490					495		
tat	gcg	tct	agc	gaa	ctt	gat	att	caa	acc	aaa	ggg	cgt	gat	ctt	tta	1536
Tyr	Ala	Ser	Ser	Glu	Leu	Asp	Ile	Gln	Thr	Lys	Gly	Arg	Asp	Leu	Leu	
			500					505					510			
ctt	gag	gat	ggg	gtt	aat	caa	cca	ctg	agt	ttc	tta	aaa	ggc	gct	tca	1584
Leu	Glu	Asp	Gly	Val	Asn	Gln	Pro	Leu	Ser	Phe	Leu	Lys	Gly	Ala	Ser	
		515					520					525				
ttg	tta	gcg	ccg	ggg	ttt	gtc	aac	act	ggg	cta	att	cac	agt	aac	ggg	1632
Leu	Leu	Ala	Pro	Gly	Phe	Val	Asn	Thr	Gly	Leu	Ile	His	Ser	Asn	Gly	
	530					535					540					
aat	gcc	aag	ctc	act	ttt	aaa	gat	gac	acc	agt	ttt	gtg	act	gaa	gga	1680
Asn	Ala	Lys	Leu	Thr	Phe	Lys	Asp	Asp	Thr	Ser	Phe	Val	Thr	Glu	Gly	
545					550					555					560	
aat	aac	ttt	atc	aca	gca	aaa	gac	aac	tta	gaa	atc	acg	gca	aaa	aat	1728
Asn	Asn	Phe	Ile	Thr	Ala	Lys	Asp	Asn	Leu	Glu	Ile	Thr	Ala	Lys	Asn	
				565					570					575		
gtt	caa	att	gat	caa	gcg	aaa	aat	att	caa	tta	aac	gcg	aat	atc	acg	1776
Val	Gln	Ile	Asp	Gln	Ala	Lys	Asn	Ile	Gln	Leu	Asn	Ala	Asn	Ile	Thr	
			580					585					590			
atc	aat	acc	aag	tct	ggg	ttt	gtg	aat	tac	ggg	acc	tta	gca	agt	gct	1824
Ile	Asn	Thr	Lys	Ser	Gly	Phe	Val	Asn	Tyr	Gly	Thr	Leu	Ala	Ser	Ala	
		595					600					605				

caa aat tta acg att aat acc gaa caa ggc agc att tat aac ata ggc	1872
Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly	
610 615 620	
ggg atc ttg ggg gcg ggt aaa agt ttg aat ctg agc gcg aaa aga gga	1920
Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly	
625 630 635 640	
gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat	1968
Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His	
645 650 655	
tct gaa ggc gcc atg aac ctc aca gcg gat cgc acg gtg tac aat tta	2016
Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu	
660 665 670	
ggg aat att ttt gct aaa ggt gac gcg acg atc aat gca aac gcg tta	2064
Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu	
675 680 685	
att aat gat gtt act ctc aca ggt cgt ctt gag tat caa gat ctg aaa	2112
Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys	
690 695 700	
aaa gat tat acg cgt tat tat cgt atc aat gaa acg gca aaa cat ggt	2160
Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly	
705 710 715 720	
tgg cat aat aac ttc tat gaa tta aac gtc gac aga gtt tct tg	2204
Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser	
725 730	

<210> 117

<211> 734

<212> PRT

<213> Pasteurella multocida

<400> 117

Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys	
1 5 10 15	
Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser	
20 25 30	
Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu	
35 40 45	
Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn	
50 55 60	
Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu	
65 70 75 80	
Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr	
85 90 95	
Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser	
100 105 110	
Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His	
115 120 125	

Gln	Thr	Lys	Ile	Lys	His	Thr	Glu	Asn	Asn	Val	Ile	Ile	Val	Asp	Ile
130						135					140				
Ala	Lys	Pro	Asn	Gln	Lys	Gly	Ile	Ser	Asp	Asn	Arg	Phe	Lys	His	Phe
145					150					155					160
Asn	Ile	Pro	Asn	Gly	Ala	Val	Phe	Asn	Asn	Ser	Ala	Lys	Glu	Lys	Arg
				165					170					175	
Ser	Gln	Leu	Val	Gly	Tyr	Leu	Pro	Gly	Asn	Gln	Asn	Leu	Thr	Glu	Gly
			180					185					190		
Ser	Glu	Ala	Lys	Ala	Ile	Leu	Asn	Gln	Val	Thr	Gly	Pro	Asp	Ala	Ser
		195					200					205			
Lys	Ile	Glu	Gly	Ala	Leu	Glu	Ile	Leu	Gly	Gln	Lys	Ala	Asp	Leu	Val
	210					215					220				
Ile	Ala	Asn	Gln	Asn	Gly	Ile	Val	Leu	Asn	Gly	Val	Lys	Thr	Ile	Asn
225					230					235					240
Ala	Asn	Arg	Phe	Val	Ala	Thr	Thr	Ser	Ser	Thr	Ile	Asp	Pro	Glu	Gln
				245					250					255	
Met	Gln	Leu	Asn	Val	Thr	Gln	Gly	Thr	Val	Thr	Ile	Gly	Val	Asp	Gly
			260					265					270		
Phe	Ala	Thr	Asp	Gly	Leu	Pro	Tyr	Leu	Asp	Ile	Ile	Ala	Lys	Lys	Ile
		275					280					285			
Glu	Gln	Lys	Gln	Ala	Ile	Thr	Lys	Glu	Arg	Thr	Gly	Asn	Ser	Glu	Thr
	290					295					300				
Asp	Ile	Thr	Phe	Val	Ala	Gly	Asn	Ser	Lys	Tyr	Asp	Leu	Lys	Thr	His
305					310					315					320
Gln	Val	Thr	Glu	Lys	His	Thr	Ala	Glu	Ala	Gln	Gly	Glu	Ile	Ala	Ile
				325					330					335	
Ser	Gly	Ala	Ser	Thr	Gly	Ala	Met	Tyr	Gly	Lys	Asn	Ile	Lys	Leu	Ile
			340					345					350		
Val	Thr	Asp	Lys	Gly	Ala	Gly	Val	Lys	His	Asp	Gly	Ile	Ile	Leu	Ser
		355					360					365			
Glu	Ala	Asp	Ile	Gln	Ile	Glu	Thr	His	Glu	Gly	Asp	Val	Glu	Leu	Gly
	370					375					380				
Asn	Thr	Lys	Asn	Asn	Gln	Asn	Glu	Asn	Tyr	Ala	Lys	Ala	His	Ala	Glu
385					390					395					400
Gly	Asn	Phe	Thr	Val	Lys	Gly	Gly	Lys	His	Val	Ile	Ile	Gly	Lys	Glu
				405					410					415	
Val	Lys	Ala	Asn	Lys	Ala	Val	Asp	Ile	Gln	Ala	Gln	Glu	Thr	Thr	Val
			420					425					430		
Arg	Gln	Asn	Ala	Lys	Leu	Thr	Ala	Lys	Thr	Ser	Ala	Lys	Ile	Thr	Ala
		435					440					445			
Ser	Lys	Ser	Val	Asn	Leu	Glu	Asp	Asn	Ala	Lys	Leu	Ile	Ala	Asn	Glu
	450					455					460				

Leu	Ser	Thr	Thr	Thr	Asn	Lys	Leu	Thr	Asn	Lys	Gly	Ser	Ile	Tyr	Gly	465	470	475	480
Lys	Lys	Val	Thr	Leu	Asp	Ala	Asp	Asn	Leu	Val	Asn	Ser	Lys	Glu	Ile	485	490	495	
Tyr	Ala	Ser	Ser	Glu	Leu	Asp	Ile	Gln	Thr	Lys	Gly	Arg	Asp	Leu	Leu	500	505	510	
Leu	Glu	Asp	Gly	Val	Asn	Gln	Pro	Leu	Ser	Phe	Leu	Lys	Gly	Ala	Ser	515	520	525	
Leu	Leu	Ala	Pro	Gly	Phe	Val	Asn	Thr	Gly	Leu	Ile	His	Ser	Asn	Gly	530	535	540	
Asn	Ala	Lys	Leu	Thr	Phe	Lys	Asp	Asp	Thr	Ser	Phe	Val	Thr	Glu	Gly	545	550	555	560
Asn	Asn	Phe	Ile	Thr	Ala	Lys	Asp	Asn	Leu	Glu	Ile	Thr	Ala	Lys	Asn	565	570	575	
Val	Gln	Ile	Asp	Gln	Ala	Lys	Asn	Ile	Gln	Leu	Asn	Ala	Asn	Ile	Thr	580	585	590	
Ile	Asn	Thr	Lys	Ser	Gly	Phe	Val	Asn	Tyr	Gly	Thr	Leu	Ala	Ser	Ala	595	600	605	
Gln	Asn	Leu	Thr	Ile	Asn	Thr	Glu	Gln	Gly	Ser	Ile	Tyr	Asn	Ile	Gly	610	615	620	
Gly	Ile	Leu	Gly	Ala	Gly	Lys	Ser	Leu	Asn	Leu	Ser	Ala	Lys	Arg	Gly	625	630	635	640
Glu	Asn	Gln	Gly	Gly	Tyr	Leu	Ile	Asn	Gln	Gly	Lys	Ser	Leu	Leu	His	645	650	655	
Ser	Glu	Gly	Ala	Met	Asn	Leu	Thr	Ala	Asp	Arg	Thr	Val	Tyr	Asn	Leu	660	665	670	
Gly	Asn	Ile	Phe	Ala	Lys	Gly	Asp	Ala	Thr	Ile	Asn	Ala	Asn	Ala	Leu	675	680	685	
Ile	Asn	Asp	Val	Thr	Leu	Thr	Gly	Arg	Leu	Glu	Tyr	Gln	Asp	Leu	Lys	690	695	700	
Lys	Asp	Tyr	Thr	Arg	Tyr	Tyr	Arg	Ile	Asn	Glu	Thr	Ala	Lys	His	Gly	705	710	715	720
Trp	His	Asn	Asn	Phe	Tyr	Glu	Leu	Asn	Val	Asp	Arg	Val	Ser			725	730		

<210> 118
 <211> 251
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> unkO

<220>
 <221> CDS
 <222> (1) .. (249)

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<400> 118
atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
  1             5             10             15

gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca 96
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
             20             25             30

tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
             35             40             45

gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga 192
Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
             50             55             60

agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240
Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
  65             70             75             80

tgt aat cat ta 251
Cys Asn His

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<210> 119
<211> 83
<212> PRT
<213> Pasteurella multocida

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<400> 119
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
  1             5             10             15

Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
             20             25             30

Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
             35             40             45

Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
             50             55             60

Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
  65             70             75             80

Cys Asn His

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<210> 120
<211> 548
<212> DNA
<213> Pasteurella multocida

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<220>
<223> unkP

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<220>
<221> CDS
<222> (1)..(546)

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<400> 120

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atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att tca	48
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser	
1 5 10 15	
aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat ttt	96
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe	
20 25 30	
gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa ggc	144
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly	
35 40 45	
atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta cgc	192
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg	
50 55 60	
acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act	240
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr	
65 70 75 80	
gca caa atc tta aaa gat acg att gca ggc gcg ttt gat tgg gca gtg	288
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val	
85 90 95	
gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc	336
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile	
100 105 110	
aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc ggt	384
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly	
115 120 125	
aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat	432
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp	
130 135 140	
gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa	480
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu	
145 150 155 160	
cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt	528
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe	
165 170 175	
tca aat cgt tta gca tcg ta	548
Ser Asn Arg Leu Ala Ser	
180	

<210> 121

<211> 182

<212> PRT

<213> Pasteurella multocida

<400> 121

Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
1 5 10 15
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
20 25 30
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
35 40 45

- 218 -

Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
50 55 60
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65 70 75 80
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
85 90 95
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
100 105 110
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
115 120 125
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
130 135 140
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145 150 155 160
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
165 170 175
Ser Asn Arg Leu Ala Ser
180

<210> 122

<211> 69

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvA-or1

<220>

<221> CDS

<222> (1)..(69)

<400> 122

atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc 48
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
1 5 10 15

gat aag ttt aag ata ctt agc 69
Asp Lys Phe Lys Ile Leu Ser
20

<210> 123

<211> 23

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 123

Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
1 5 10 15

Asp Lys Phe Lys Ile Leu Ser
20

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<210> 124
<211> 64
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> apvA-or2

<220>
<221> CDS
<222> (3)..(62)

<400> 124
ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta      47
  Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu
    1             5             10             15

ttg gca agc atg aca ta                                              64
  Leu Ala Ser Met Thr
                20

<210> 125
<211> 20
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 125
Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu
  1             5             10             15

Ala Ser Met Thr
      20

<210> 126
<211> 653
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> apvB

<220>
<221> CDS
<222> (1)..(651)

<400> 126
tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc      48
Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
  1             5             10             15

gaa att gga ttg gga gga gcc cgt gag agt agt att tac tat tct aaa      96
Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
      20             25             30

cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt      144
His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
      35             40             45

aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa      192
Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
      50             55             60

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- 220 -

caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt 240
Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
65 70 75 80

gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt 288
Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
85 90 95

att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat 336
Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
100 105 110

aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa 384
Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
115 120 125

gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa 432
Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
130 135 140

tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca 480
Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
145 150 155 160

agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa 528
Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
165 170 175

tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct 576
Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
180 185 190

tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat 624
Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
195 200 205

ctt ggc atg ggt tta tct gtc ggt tgg at 653
Leu Gly Met Gly Leu Ser Val Gly Trp
210 215

<210> 127

<211> 217

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 127

Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
1 5 10 15

Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
20 25 30

His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
35 40 45

Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
50 55 60

Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
65 70 75 80

Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser

85					90					95					
Ile	Gln	Thr	Arg	Lys	Thr	Gln	Phe	Ala	Phe	Gly	Trp	Gly	Leu	Asn	Tyr
			100					105					110		
Asn	Leu	Gly	Gly	Leu	Phe	Gly	Leu	Asn	Asp	Thr	Phe	Ile	Ser	Leu	Glu
		115					120					125			
Gly	Lys	Ser	Gly	Lys	Arg	Gly	Ala	Ser	Ser	Asn	Val	Ser	Leu	Leu	Lys
	130					135					140				
Ser	Phe	Asn	Met	Thr	Lys	Asn	Trp	Lys	Val	Ser	Pro	Tyr	Ile	Gly	Ser
145						150					155				160
Ser	Tyr	Tyr	Ser	Ser	Lys	Tyr	Thr	Asp	Tyr	Tyr	Phe	Gly	Ile	Lys	Gln
				165					170					175	
Ser	Glu	Leu	Gly	Asn	Lys	Ile	Thr	Ser	Val	Tyr	Lys	Pro	Lys	Ala	Ala
			180					185					190		
Tyr	Ala	Thr	His	Ile	Gly	Ile	Asn	Thr	Asp	Tyr	Ala	Phe	Thr	Asn	Asn
		195					200					205			
Leu	Gly	Met	Gly	Leu	Ser	Val	Gly	Trp							
	210					215									

<210> 128
 <211> 242
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> apvC

<220>
 <221> CDS
 <222> (1)..(240)

<400> 128																
atg	tgg	cgg	atg	gga	gat	ttt	atg	tct	aaa	aaa	gag	agg	ctg	aat	gat	48
Met	Trp	Arg	Met	Gly	Asp	Phe	Met	Ser	Lys	Lys	Glu	Arg	Leu	Asn	Asp	
1				5					10					15		
<400> 96																
atg	gct	cgc	cag	att	tta	tca	gcg	gcg	gag	ttg	ctc	att	gca	aag	gaa	96
Met	Ala	Arg	Gln	Ile	Leu	Ser	Ala	Ala	Glu	Leu	Leu	Ile	Ala	Lys	Glu	
			20						25				30			
<400> 144																
ggt	ttg	caa	aat	tta	tcg	atg	agg	aaa	atc	gca	agt	gaa	gcc	ggt	atc	144
Gly	Leu	Gln	Asn	Leu	Ser	Met	Arg	Lys	Ile	Ala	Ser	Glu	Ala	Gly	Ile	
		35					40					45				
<400> 192																
gca	aca	ggc	acg	ctt	tat	ctc	tat	ttc	aaa	acg	aaa	gac	gag	tta	ctg	192
Ala	Thr	Gly	Thr	Leu	Tyr	Leu	Tyr	Phe	Lys	Thr	Lys	Asp	Glu	Leu	Leu	
	50					55					60					
<400> 240																
gat	tgt	ttg	gcg	gaa	caa	tta	cat	gaa	cga	tat	tat	cgt	tat	ctg	aat	240
Asp	Cys	Leu	Ala	Glu	Gln	Leu	His	Glu	Arg	Tyr	Tyr	Arg	Tyr	Leu	Asn	
65					70					75					80	
at															242	

<210> 129

<211> 80

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 129

Met	Trp	Arg	Met	Gly	Asp	Phe	Met	Ser	Lys	Lys	Glu	Arg	Leu	Asn	Asp
1				5					10					15	
Met	Ala	Arg	Gln	Ile	Leu	Ser	Ala	Ala	Glu	Leu	Leu	Ile	Ala	Lys	Glu
			20					25					30		
Gly	Leu	Gln	Asn	Leu	Ser	Met	Arg	Lys	Ile	Ala	Ser	Glu	Ala	Gly	Ile
		35					40					45			
Ala	Thr	Gly	Thr	Leu	Tyr	Leu	Tyr	Phe	Lys	Thr	Lys	Asp	Glu	Leu	Leu
	50					55					60				
Asp	Cys	Leu	Ala	Glu	Gln	Leu	His	Glu	Arg	Tyr	Tyr	Arg	Tyr	Leu	Asn
65					70					75					80

<210> 130

<211> 527

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvD

<220>

<221> CDS

<222> (1) .. (525)

<400> 130

aat	att	caa	aaa	aca	gtt	att	gct	agc	ggc	aca	ttg	caa	gcg	act	gaa	48
Asn	Ile	Gln	Lys	Thr	Val	Ile	Ala	Ser	Gly	Thr	Leu	Gln	Ala	Thr	Glu	
1				5					10					15		
caa	gta	gat	att	ggg	gca	caa	gta	tct	ggg	cag	att	aag	cat	att	tta	96
Gln	Val	Asp	Ile	Gly	Ala	Gln	Val	Ser	Gly	Gln	Ile	Lys	His	Ile	Leu	
			20					25					30			
gta	caa	gaa	gga	cag	aag	gtt	aaa	aaa	ggg	gag	cta	tta	gct	gta	att	144
Val	Gln	Glu	Gly	Gln	Lys	Val	Lys	Lys	Gly	Glu	Leu	Leu	Ala	Val	Ile	
		35					40					45				
gat	cca	cgt	ctg	gct	gaa	acg	gaa	tta	aaa	cta	gca	aaa	gct	gag	cta	192
Asp	Pro	Arg	Leu	Ala	Glu	Thr	Glu	Leu	Lys	Leu	Ala	Lys	Ala	Glu	Leu	
	50					55					60					
gca	aat	gct	tct	gct	aat	ttg	gat	aca	aaa	aaa	att	aat	ctt	aag	caa	240
Ala	Asn	Ala	Ser	Ala	Asn	Leu	Asp	Thr	Lys	Lys	Ile	Asn	Leu	Lys	Gln	
65					70					75					80	
ctg	caa	tca	gat	tgg	gaa	cgt	cat	caa	cgt	ttg	ata	cga	acc	aat	gcg	288
Leu	Gln	Ser	Asp	Trp	Glu	Arg	His	Gln	Arg	Leu	Ile	Arg	Thr	Asn	Ala	
			85						90					95		
aca	agc	caa	aag	gaa	aca	gaa	gaa	gca	aaa	agt	aga	tta	aat	acg	gcc	336
Thr	Ser	Gln	Lys	Glu	Thr	Glu	Glu	Ala	Lys	Ser	Arg	Leu	Asn	Thr	Ala	
			100					105						110		

aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc 384
Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
115 120 125

aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct 432
Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
130 135 140

cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act 480
Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
145 150 155 160

tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at 527
Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
165 170 175

<210> 131

<211> 175

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 131

Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
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Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
20 25 30

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
35 40 45

Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
50 55 60

Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
65 70 75 80

Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
85 90 95

Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
100 105 110

Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
115 120 125

Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
130 135 140

Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
145 150 155 160

Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
165 170 175

<210> 132

<211> 867

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> atpG

<220>

<221> CDS

<222> (1)..(864)

<400> 132

atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat	48
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn	
1 5 10 15	
act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg	96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met	
20 25 30	
cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca	144
Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr	
35 40 45	
atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag	192
Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys	
50 55 60	
cac ccg ttt tta act gaa cgt gat att aaa aaa gta ggc tat ctt gtc	240
His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val	
65 70 75 80	
gtt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc	288
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe	
85 90 95	
aaa gcg act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt	336
Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser	
100 105 110	
gtt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat	384
Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn	
115 120 125	
cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg	432
Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro	
130 135 140	
gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat gcg ttc	480
Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe	
145 150 155 160	
cga aac gga gaa gtg gat gcg gtt tac gtc gct tac aac cgt ttt gaa	528
Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu	
165 170 175	
aat acg atg tca caa aaa cct gtt atc gca cag tta ctt ccg tta cct	576
Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro	
180 185 190	
aaa cta gat gac gat gaa tta gat acg aaa ggt tca tgg gat tat att	624
Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile	
195 200 205	
tat gaa ccg aat cca caa gtt tta ttg gat agt tta ctt gtt cgt tat	672
Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr	
210 215 220	

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<210> 133
<211> 288
<212> PRT
<213> Actinobacillus pleuropneumoniae
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Thr	Gln	Lys	Ile	Thr	Lys	Ala	Met	Glu	Met	Val	Ala	Thr	Ser	Lys	Met
			20					25					30		
Arg	Lys	Thr	Gln	Glu	Arg	Met	Ala	Ala	Ser	Arg	Pro	Tyr	Ser	Glu	Thr
		35					40					45			
Ile	Arg	Lys	Val	Ile	Ser	His	Ile	Ala	Lys	Gly	Ser	Ile	Gly	Tyr	Lys
50						55					60				
His	Pro	Phe	Leu	Thr	Glu	Arg	Asp	Ile	Lys	Lys	Val	Gly	Tyr	Leu	Val
65					70					75					80
Val	Ser	Thr	Asp	Arg	Gly	Leu	Cys	Gly	Gly	Leu	Asn	Ile	Asn	Leu	Phe
				85					90					95	
Lys	Ala	Thr	Leu	Asn	Glu	Phe	Lys	Thr	Trp	Lys	Asp	Lys	Asp	Val	Ser
			100					105					110		
Val	Glu	Leu	Gly	Leu	Val	Gly	Ser	Lys	Gly	Val	Ser	Phe	Tyr	Gln	Asn
		115					120					125			
Leu	Gly	Leu	Asn	Val	Arg	Ser	Gln	Val	Thr	Gly	Leu	Gly	Asp	Asn	Pro
130						135					140				
Glu	Met	Glu	Arg	Ile	Val	Gly	Ala	Val	Asn	Glu	Met	Ile	Asn	Ala	Phe
145					150					155					160
Arg	Asn	Gly	Glu	Val	Asp	Ala	Val	Tyr	Val	Ala	Tyr	Asn	Arg	Phe	Glu
				165					170					175	
Asn	Thr	Met	Ser	Gln	Lys	Pro	Val	Ile	Ala	Gln	Leu	Leu	Pro	Leu	Pro
			180					185					190		
Lys	Leu	Asp	Asp	Asp	Glu	Leu	Asp	Thr	Lys	Gly	Ser	Trp	Asp	Tyr	Ile
		195					200					205			

Tyr	Glu	Pro	Asn	Pro	Gln	Val	Leu	Leu	Asp	Ser	Leu	Leu	Val	Arg	Tyr
210						215					220				
Leu	Glu	Thr	Gln	Val	Tyr	Gln	Ala	Val	Val	Asp	Asn	Leu	Ala	Ser	Glu
225					230					235					240
Gln	Ala	Ala	Arg	Met	Val	Ala	Met	Lys	Ala	Ala	Thr	Asp	Asn	Ala	Gly
				245					250					255	
Thr	Leu	Ile	Asp	Glu	Leu	Gln	Leu	Val	Tyr	Asn	Lys	Ala	Arg	Gln	Ala
			260					265						270	
Ser	Ile	Thr	Asn	Glu	Leu	Asn	Glu	Ile	Val	Ala	Gly	Ala	Ala	Ala	Ile
		275					280					285			

<210> 134

<211> 534

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> atpH

<220>

<221> CDS

<222> (1)..(531)

<400> 134

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Met	Ser	Glu	Leu	Ser	Thr	Val	Ala	Arg	Pro	Tyr	Ala	Lys	Ala	Ala	Phe	
1				5					10					15		
gat	ttt	gct	tta	gaa	caa	ggg	cag	ttg	gac	aaa	tgg	caa	gaa	atg	tta	96
Asp	Phe	Ala	Leu	Glu	Gln	Gly	Gln	Leu	Asp	Lys	Trp	Gln	Glu	Met	Leu	
			20					25					30			
cag	ttt	tcg	gca	ttc	gtt	gct	gaa	aac	gaa	caa	gtg	gcg	gaa	tat	att	144
Gln	Phe	Ser	Ala	Phe	Val	Ala	Glu	Asn	Glu	Gln	Val	Ala	Glu	Tyr	Ile	
		35					40					45				
aat	tct	tcc	ctt	gca	agc	ggg	cag	att	tct	gaa	act	ttt	atc	aaa	atc	192
Asn	Ser	Ser	Leu	Ala	Ser	Gly	Gln	Ile	Ser	Glu	Thr	Phe	Ile	Lys	Ile	
	50					55					60					
tgc	ggc	gac	caa	ctt	gat	caa	tat	ggg	caa	aat	ttt	att	cgt	gta	atg	240
Cys	Gly	Asp	Gln	Leu	Asp	Gln	Tyr	Gly	Gln	Asn	Phe	Ile	Arg	Val	Met	
65					70					75				80		
gct	gaa	aat	aaa	cgt	ctg	gct	gtg	ttg	cct	atg	gtt	ttt	gat	act	ttc	288
Ala	Glu	Asn	Lys	Arg	Leu	Ala	Val	Leu	Pro	Met	Val	Phe	Asp	Thr	Phe	
			85						90					95		
gta	tca	tta	cga	gcg	gaa	cat	gaa	gcg	gta	aaa	gat	gta	aca	att	gtt	336
Val	Ser	Leu	Arg	Ala	Glu	His	Glu	Ala	Val	Lys	Asp	Val	Thr	Ile	Val	
			100					105						110		
tcg	gca	aac	gaa	tta	agt	caa	gca	caa	gaa	gat	aaa	atc	gca	aaa	gcg	384
Ser	Ala	Asn	Glu	Leu	Ser	Gln	Ala	Gln	Glu	Asp	Lys	Ile	Ala	Lys	Ala	
		115					120					125				
atg	gaa	aaa	cgc	tta	ggg	caa	aaa	gtt	cgt	tta	acc	aac	caa	atc	gat	432
Met	Glu	Lys	Arg	Leu	Gly	Gln	Lys	Val	Arg	Leu	Thr	Asn	Gln	Ile	Asp	

130	135	140	
aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att			480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile			
145	150	155	160
gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc			528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser			
	165	170	175
ttg taa			534
Leu			

<210> 135
 <211> 177
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 135
 Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1 5 10 15
 Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
 20 25 30
 Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
 35 40 45
 Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
 50 55 60
 Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
 65 70 75 80
 Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
 85 90 95
 Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
 100 105 110
 Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
 115 120 125
 Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
 130 135 140
 Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
 145 150 155 160
 Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
 165 170 175
 Leu

<210> 136
 <211> 321
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>

<223> dksA

<220>

<221> CDS

<222> (1)..(318)

<400> 136

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gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa 48
Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1          5          10          15

atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act 96
Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
          20          25          30

cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt 144
Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
          35          40          45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac 192
Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
          50          55          60

gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt 240
Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
 65          70          75          80

tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt 288
Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
          85          90          95

gcg gaa atc cgt gaa aag caa atg ggc tta taa 321
Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
          100          105

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<210> 137

<211> 106

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 137

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Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1          5          10          15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
          20          25          30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
          35          40          45

Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
          50          55          60

Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
          65          70          75          80

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
          85          90          95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
          100          105

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<210> 138
<211> 33
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> dnaK

<220>
<221> CDS
<222> (1)..(30)

<400> 138
gct gag ttt gaa gaa gtg aaa gat aat aaa taa 33
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
1 5 10

<210> 139
<211> 10
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 139
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
1 5 10

<210> 140
<211> 453
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> exbB

<220>
<221> CDS
<222> (1)..(450)

<400> 140
atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
1 5 10 15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96
Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
20 25 30

gaa cgc gta ctt ttc tac aaa caa ttg gat gtg acc aaa tat gac acg 144
Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
35 40 45

cta caa gat ttg gaa att gat acc act cgc aat tta acc acc att tcc 192
Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
50 55 60

act atc ggt gcc aac gcc cct tat atc ggt tta tta gga acc gta tta 240
Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
65 70 75 80

ggg atc tta ctt acc ttc tat cat tta ggg cat tcc ggc ggt gat att 288
Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile

85								90				95				
gac	gcc	gca	tcc	att	atg	gtt	cac	ctt	tcg	ctt	gca	tta	aaa	gca	acc	336
Asp	Ala	Ala	Ser	Ile	Met	Val	His	Leu	Ser	Leu	Ala	Leu	Lys	Ala	Thr	
			100					105					110			
gca	gcc	ggg	atc	tta	gtc	gct	att	ccg	gca	atg	atg	ttc	tac	agc	ggg	384
Ala	Ala	Gly	Ile	Leu	Val	Ala	Ile	Pro	Ala	Met	Met	Phe	Tyr	Ser	Gly	
		115					120					125				
ttt	aac	cgt	aaa	gtg	gat	gaa	agc	aaa	ctt	aaa	tgg	caa	gcg	att	caa	432
Phe	Asn	Arg	Lys	Val	Asp	Glu	Ser	Lys	Leu	Lys	Trp	Gln	Ala	Ile	Gln	
	130					135					140					
gct	cgt	aaa	gcc	aat	caa	taa										453
Ala	Arg	Lys	Ala	Asn	Gln											
145					150											

<210> 141
 <211> 150
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 141																	
Met	Glu	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	His	Val	Asp	Tyr	Ile	Ile		
1				5					10					15			
Leu	Gly	Leu	Leu	Leu	Leu	Met	Ser	Val	Val	Leu	Val	Trp	Lys	Ile	Ile		
			20					25					30				
Glu	Arg	Val	Leu	Phe	Tyr	Lys	Gln	Leu	Asp	Val	Thr	Lys	Tyr	Asp	Thr		
		35					40					45					
Leu	Gln	Asp	Leu	Glu	Ile	Asp	Thr	Thr	Arg	Asn	Leu	Thr	Thr	Ile	Ser		
	50					55					60						
Thr	Ile	Gly	Ala	Asn	Ala	Pro	Tyr	Ile	Gly	Leu	Leu	Gly	Thr	Val	Leu		
	65				70					75					80		
Gly	Ile	Leu	Leu	Thr	Phe	Tyr	His	Leu	Gly	His	Ser	Gly	Gly	Asp	Ile		
				85					90					95			
Asp	Ala	Ala	Ser	Ile	Met	Val	His	Leu	Ser	Leu	Ala	Leu	Lys	Ala	Thr		
			100					105					110				
Ala	Ala	Gly	Ile	Leu	Val	Ala	Ile	Pro	Ala	Met	Met	Phe	Tyr	Ser	Gly		
		115					120					125					
Phe	Asn	Arg	Lys	Val	Asp	Glu	Ser	Lys	Leu	Lys	Trp	Gln	Ala	Ile	Gln		
	130					135					140						
Ala	Arg	Lys	Ala	Asn	Gln												
145					150												

<210> 142
 <211> 720
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> fkpA

<220>

<221> CDS

<222> (1)..(717)

<400> 142

atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc	48
Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe	
1 5 10 15	
gtt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat	96
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp	
20 25 30	
tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc	144
Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val	
35 40 45	
gtt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg	192
Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu	
50 55 60	
gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa	240
Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu	
65 70 75 80	
gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa	288
Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln	
85 90 95	
gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt	336
Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly	
100 105 110	
aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc	384
Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr	
115 120 125	
gct tcc ggt tta ctt tat aaa att gaa aaa gcc ggc acg ggc gaa tcg	432
Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser	
130 135 140	
cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc	480
Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr	
145 150 155 160	
gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa	528
Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu	
165 170 175	
ttc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg	576
Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met	
180 185 190	
ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt	624
Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly	
195 200 205	
tac ggc gaa cgc caa gca ggt aag att ccg gca agt tca acc tta aaa	672
Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys	
210 215 220	
ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa	720
Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys	

225

230

235

<210> 143

<211> 239

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 143

Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
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Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
20 25 30

Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
35 40 45

Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
50 55 60

Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu
65 70 75 80

Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
85 90 95

Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
100 105 110

Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
115 120 125

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
130 135 140

Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
145 150 155 160

Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
165 170 175

Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
180 185 190

Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
195 200 205

Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
210 215 220

Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
225 230 235

<210> 144

<211> 290

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> HI0379

<220>

<221> CDS

<222> (3)..(287)

<400> 144

tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa	47
His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln	
1 5 10 15	
cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat	95
Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn	
20 25 30	
ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct	143
Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser	
35 40 45	
cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt	191
Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly	
50 55 60	
gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg	239
Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser	
65 70 75	
gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat	287
Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His	
80 85 90 95	
taa	290

<210> 145

<211> 95

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 145

His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln Pro	
1 5 10 15	
Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn Leu	
20 25 30	
Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser Gln	
35 40 45	
Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly Val	
50 55 60	
Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser Asp	
65 70 75 80	
His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His	
85 90 95	

<210> 146

<211> 273

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> hupA

<220>

<221> CDS

<222> (1)..(270)

<400> 146

atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta	48
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu	
1 5 10 15	
agc aag aaa gac gcg aaa gcg gca tta gaa gcg act tta aat gcg atc	96
Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile	
20 25 30	
tct gaa agc cta aaa aat ggc gac acc gtt cag tta atc ggc ttc ggt	144
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly	
35 40 45	
act ttt aaa gta aac gag cgt aat gca cgt acg ggt cgt aac ccg cgt	192
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg	
50 55 60	
acc ggc gaa gaa atc aaa atc gca gca tct aaa gtg ccg gcg ttt gtt	240
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val	
65 70 75 80	
gca ggt aaa gca tta aaa gat tta gta aaa taa	273
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys	
85 90	

<210> 147

<211> 90

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 147

Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu	
1 5 10 15	
Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile	
20 25 30	
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly	
35 40 45	
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg	
50 55 60	
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val	
65 70 75 80	
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys	
85 90	

<210> 148

<211> 551

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> lpdA

<220>

<221> CDS

<222> (1)..(549)

<400> 148

atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct	48
Met Ser Lys Glu Ile Lys Thr Gln Val Val Leu Gly Ala Gly Pro	
1 5 10 15	
gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca	96
Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr	
20 25 30	
gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta	144
Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val	
35 40 45	
ggt tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa	192
Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu	
50 55 60	
gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac	240
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn	
65 70 75 80	
att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa	288
Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys	
85 90 95	
tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta	336
Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val	
100 105 110	
gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt	384
Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg	
115 120 125	
gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att	432
Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile	
130 135 140	
gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat	480
Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp	
145 150 155 160	
ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc	528
Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro	
165 170 175	
gaa aaa att act cat tat ggg cc	551
Glu Lys Ile Thr His Tyr Gly	
180	

<210> 149

<211> 183

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 149

Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro

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Ala Gly Tyr	Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr		
	20	25	30
Val Ile Val	Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val		
	35	40	45
Gly Cys Ile	Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu		
	50	55	60
Glu Ala Lys	His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn		
	65	70	75
Ile Asp Leu	Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys		
	85	90	95
Leu Thr Gly	Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val		
	100	105	110
Val Glu Gly	Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg		
	115	120	125
Asp Arg Asp	Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile		
	130	135	140
Ala Ala Gly	Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp		
	145	150	155
Pro Arg Val	Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro		
	165	170	175
Glu Lys Ile	Thr His Tyr Gly		
	180		

<210> 150
 <211> 1095
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> Omp5-2

<220>
 <221> CDS
 <222> (1) .. (1092)

<400> 150	
atg aaa aaa tca tta gtt gct tta aca gta tta tcg gct gca gcg gta	48
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val	
1 5 10 15	
gct caa gca gcg cca caa caa aat act ttc tac gca ggt gcg aaa gca	96
Ala Gln Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala	
20 25 30	
ggg tgg gcg tca ttc cat gat ggt atc gaa caa tta gat tca gct aaa	144
Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys	
35 40 45	
aac aca gat cgc ggt aca aaa tac ggt atc aac cgt aat tca gta act	192
Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr	

50	55	60	
tac ggc gta ttc ggc ggt tac caa att tta aac caa gac aaa tta ggt Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly 65 70 75 80			240
tta gcg gct gaa tta ggt tat gac tat ttc ggt cgt gtg cgc ggt tct Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser 85 90 95			288
gaa aaa cca aac ggt aaa gcg gac aag aaa act ttc cgt cac gct gca Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala 100 105 110			336
cac ggt gcg aca atc gca tta aaa cct agc tac gaa gta tta cct gac His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp 115 120 125			384
tta gac gtt tac ggt aaa gta ggt atc gca tta gta aac aat aca tat Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr 130 135 140			432
aaa aca ttc aat gca gca caa gag aaa gtg aaa act cgt cgt ttc caa Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln 145 150 155 160			480
agt tct tta att tta ggt gcg ggt gtt gag tac gca att ctt cct gaa Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu 165 170 175			528
tta gcg gca cgt gtt gaa tac caa tgg tta aac aac gca ggt aaa gca Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala 180 185 190			576
agc tac tct act tta aat cgt atg ggt gca act gac tac cgt tcg gat Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp 195 200 205			624
atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala 210 215 220			672
gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser 225 230 235 240			720
tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala 245 250 255			768
gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu 260 265 270			816
tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys 275 280 285			864
gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala 290 295 300			912
aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta			960

Asn	Tyr	Ile	Val	Ser	Lys	Gly	Ala	Pro	Ala	Ala	Asn	Val	Thr	Ala	Val	
305					310					315					320	
ggt	tac	ggt	gaa	gca	aac	cct	gta	acc	ggc	gca	aca	tgt	gac	aaa	gtt	1008
Gly	Tyr	Gly	Glu	Ala	Asn	Pro	Val	Thr	Gly	Ala	Thr	Cys	Asp	Lys	Val	
				325					330					335		
aaa	ggt	cgt	aaa	gca	tta	atc	gct	tgc	tta	gca	ccg	gat	cgt	cgt	gtt	1056
Lys	Gly	Arg	Lys	Ala	Leu	Ile	Ala	Cys	Leu	Ala	Pro	Asp	Arg	Arg	Val	
			340					345					350			
gaa	gtt	caa	gtt	caa	ggt	act	aaa	gaa	gta	act	atg	taa				1095
Glu	Val	Gln	Val	Gln	Gly	Thr	Lys	Glu	Val	Thr	Met					
		355					360									

<210> 151

<211> 364

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 151

Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Thr	Val	Leu	Ser	Ala	Ala	Ala	Val	
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			20					25					30			
Gly	Trp	Ala	Ser	Phe	His	Asp	Gly	Ile	Glu	Gln	Leu	Asp	Ser	Ala	Lys	
		35					40					45				
Asn	Thr	Asp	Arg	Gly	Thr	Lys	Tyr	Gly	Ile	Asn	Arg	Asn	Ser	Val	Thr	
		50				55					60					
Tyr	Gly	Val	Phe	Gly	Gly	Tyr	Gln	Ile	Leu	Asn	Gln	Asp	Lys	Leu	Gly	
	65				70					75					80	
Leu	Ala	Ala	Glu	Leu	Gly	Tyr	Asp	Tyr	Phe	Gly	Arg	Val	Arg	Gly	Ser	
			85						90					95		
Glu	Lys	Pro	Asn	Gly	Lys	Ala	Asp	Lys	Lys	Thr	Phe	Arg	His	Ala	Ala	
			100					105					110			
His	Gly	Ala	Thr	Ile	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp	
		115					120					125				
Leu	Asp	Val	Tyr	Gly	Lys	Val	Gly	Ile	Ala	Leu	Val	Asn	Asn	Thr	Tyr	
	130					135					140					
Lys	Thr	Phe	Asn	Ala	Ala	Gln	Glu	Lys	Val	Lys	Thr	Arg	Arg	Phe	Gln	
	145				150					155					160	
Ser	Ser	Leu	Ile	Leu	Gly	Ala	Gly	Val	Glu	Tyr	Ala	Ile	Leu	Pro	Glu	
				165					170					175		
Leu	Ala	Ala	Arg	Val	Glu	Tyr	Gln	Trp	Leu	Asn	Asn	Ala	Gly	Lys	Ala	
			180					185					190			
Ser	Tyr	Ser	Thr	Leu	Asn	Arg	Met	Gly	Ala	Thr	Asp	Tyr	Arg	Ser	Asp	
		195					200					205				
Ile	Ser	Ser	Val	Ser	Ala	Gly	Leu	Ser	Tyr	Arg	Phe	Gly	Gln	Gly	Ala	
	210					215					220					

Ala	Pro	Val	Ala	Ala	Pro	Ala	Val	Glu	Thr	Lys	Asn	Phe	Ala	Phe	Ser
225					230					235					240
Ser	Asp	Val	Leu	Phe	Ala	Phe	Gly	Lys	Ser	Asn	Leu	Lys	Pro	Ala	Ala
				245					250					255	
Ala	Thr	Ala	Leu	Asp	Ala	Met	Gln	Thr	Glu	Ile	Asn	Asn	Ala	Gly	Leu
			260					265					270		
Ser	Asn	Ala	Ala	Ile	Gln	Val	Asn	Gly	Tyr	Thr	Asp	Arg	Ile	Gly	Lys
		275					280					285			
Glu	Ala	Ser	Asn	Leu	Lys	Leu	Ser	Gln	Arg	Arg	Ala	Glu	Thr	Val	Ala
	290					295					300				
Asn	Tyr	Ile	Val	Ser	Lys	Gly	Ala	Pro	Ala	Ala	Asn	Val	Thr	Ala	Val
305					310					315					320
Gly	Tyr	Gly	Glu	Ala	Asn	Pro	Val	Thr	Gly	Ala	Thr	Cys	Asp	Lys	Val
				325					330					335	
Lys	Gly	Arg	Lys	Ala	Leu	Ile	Ala	Cys	Leu	Ala	Pro	Asp	Arg	Arg	Val
			340					345					350		
Glu	Val	Gln	Val	Gln	Gly	Thr	Lys	Glu	Val	Thr	Met				
		355					360								

<210> 152

<211> 1110

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> Omp5

<220>

<221> CDS

<222> (1)..(1107)

<400> 152

atg	aaa	aaa	tca	tta	ggt	gct	tta	gca	gta	tta	tcg	gct	gca	gca	gta	48
Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Ala	Val	Leu	Ser	Ala	Ala	Ala	Val	
1				5					10					15		
gct	caa	gca	gct	cca	caa	caa	aat	act	ttc	tac	gca	ggt	gca	aaa	ggt	96
Ala	Gln	Ala	Ala	Pro	Gln	Gln	Asn	Thr	Phe	Tyr	Ala	Gly	Ala	Lys	Val	
			20					25					30			
ggt	caa	tca	tca	ttt	cac	cac	ggt	ggt	aac	caa	tta	aaa	tct	ggt	cac	144
Gly	Gln	Ser	Ser	Phe	His	His	Gly	Val	Asn	Gln	Leu	Lys	Ser	Gly	His	
		35					40					45				
gat	gat	cgt	tat	aat	gat	aaa	aca	cgt	aag	tat	ggt	atc	aac	cgt	aac	192
Asp	Asp	Arg	Tyr	Asn	Asp	Lys	Thr	Arg	Lys	Tyr	Gly	Ile	Asn	Arg	Asn	
		50				55					60					
tct	gta	act	tac	ggt	gta	ttc	ggc	ggt	tac	caa	atc	tta	aac	caa	aat	240
Ser	Val	Thr	Tyr	Gly	Val	Phe	Gly	Gly	Tyr	Gln	Ile	Leu	Asn	Gln	Asn	
	65				70				75						80	
aac	ttc	ggt	tta	gca	gct	gaa	tta	ggc	tat	gac	tac	tac	ggt	cgc	gta	288
Asn	Phe	Gly	Leu	Ala	Ala	Glu	Leu	Gly	Tyr	Asp	Tyr	Tyr	Gly	Arg	Val	

85								90								95	
cgt	ggt	aac	gta	gat	gaa	ttc	cgt	aca	ggt	aaa	cac	tct	gct	cac	ggt	336	
Arg	Gly	Asn	Val	Asp	Glu	Phe	Arg	Thr	Val	Lys	His	Ser	Ala	His	Gly		
100								105								110	
tta	aac	tta	gcg	tta	aaa	cca	agc	tac	gaa	gta	tta	cct	gac	tta	gac	384	
Leu	Asn	Leu	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp	Leu	Asp		
115								120								125	
ggt	tac	ggt	aaa	gta	ggt	att	gcg	ggt	ggt	cgt	aat	gac	tat	aaa	aaa	432	
Val	Tyr	Gly	Lys	Val	Gly	Ile	Ala	Val	Val	Arg	Asn	Asp	Tyr	Lys	Lys		
130								135								140	
tat	ggt	gcg	gaa	aac	act	aac	gaa	tca	aca	aca	aaa	ttc	cac	aaa	tta	480	
Tyr	Gly	Ala	Glu	Asn	Thr	Asn	Glu	Ser	Thr	Thr	Lys	Phe	His	Lys	Leu		
145								150								155	
aaa	gca	tca	act	att	tta	ggt	gca	ggt	ggt	gag	tac	gca	att	ctt	cct	528	
Lys	Ala	Ser	Thr	Ile	Leu	Gly	Ala	Gly	Val	Glu	Tyr	Ala	Ile	Leu	Pro		
165								170								175	
gaa	tta	gcg	gca	cgt	ggt	gaa	tac	caa	tac	tta	aac	aaa	gcg	ggt	aac	576	
Glu	Leu	Ala	Ala	Arg	Val	Glu	Tyr	Gln	Tyr	Leu	Asn	Lys	Ala	Gly	Asn		
180								185								190	
tta	aat	aaa	gca	tta	ggt	cgt	tca	ggc	aca	caa	gat	gtg	gac	ttc	caa	624	
Leu	Asn	Lys	Ala	Leu	Val	Arg	Ser	Gly	Thr	Gln	Asp	Val	Asp	Phe	Gln		
195								200								205	
tat	gct	cct	gat	atc	cac	tct	gta	aca	gca	ggt	tta	tca	tac	cgt	ttc	672	
Tyr	Ala	Pro	Asp	Ile	His	Ser	Val	Thr	Ala	Gly	Leu	Ser	Tyr	Arg	Phe		
210								215								220	
ggt	caa	ggc	gct	gta	gca	cca	ggt	ggt	gag	cca	gaa	ggt	gta	act	aaa	720	
Gly	Gln	Gly	Ala	Val	Ala	Pro	Val	Val	Glu	Pro	Glu	Val	Val	Thr	Lys		
225								230								235	
aac	ttc	gca	ttc	agc	tca	gac	ggt	tta	ttt	gat	ttc	ggt	aaa	tca	agc	768	
Asn	Phe	Ala	Phe	Ser	Ser	Asp	Val	Leu	Phe	Asp	Phe	Gly	Lys	Ser	Ser		
245								250								255	
tta	aaa	cca	gca	gca	gca	aca	gct	tta	gac	gca	gct	aac	act	gaa	atc	816	
Leu	Lys	Pro	Ala	Ala	Ala	Thr	Ala	Leu	Asp	Ala	Ala	Asn	Thr	Glu	Ile		
260								265								270	
gct	aac	tta	ggt	tta	gca	act	cca	gct	atc	caa	ggt	aac	ggt	tat	aca	864	
Ala	Asn	Leu	Gly	Leu	Ala	Thr	Pro	Ala	Ile	Gln	Val	Asn	Gly	Tyr	Thr		
275								280								285	
gac	cgt	atc	ggt	aaa	gaa	gct	tca	aac	tta	aaa	ctt	tca	caa	cgc	cgt	912	
Asp	Arg	Ile	Gly	Lys	Glu	Ala	Ser	Asn	Leu	Lys	Leu	Ser	Gln	Arg	Arg		
290								295								300	
gca	gaa	act	gta	gct	aac	tac	tta	ggt	tct	aaa	ggt	caa	aac	cct	gca	960	
Ala	Glu	Thr	Val	Ala	Asn	Tyr	Leu	Val	Ser	Lys	Gly	Gln	Asn	Pro	Ala		
305								310								315	
aac	gta	act	gca	gta	ggt	tac	ggt	gaa	gca	aac	cca	gta	acc	ggc	gca	1008	
Asn	Val	Thr	Ala	Val	Gly	Tyr	Gly	Glu	Ala	Asn	Pro	Val	Thr	Gly	Ala		
325								330								335	
aca	tgt	gat	gca	ggt	aaa	ggt	cgt	aaa	gca	tta	atc	gct	tgc	tta	gca	1056	

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Thr	Cys	Asp	Ala	Val	Lys	Gly	Arg	Lys	Ala	Leu	Ile	Ala	Cys	Leu	Ala		
			340					345					350				
ccg	gat	cgt	cgt	gtt	gaa	gtt	caa	gta	caa	ggg	gct	aaa	aac	gta	gct	1104	
Pro	Asp	Arg	Arg	Val	Glu	Val	Gln	Val	Gln	Gly	Ala	Lys	Asn	Val	Ala		
		355					360					365					
atg	taa															1110	
Met																	
<210> 153																	
<211> 369																	
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<213> Actinobacillus pleuropneumoniae																	
<400> 153																	
Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Ala	Val	Leu	Ser	Ala	Ala	Ala	Val		
1				5					10					15			
Ala	Gln	Ala	Ala	Pro	Gln	Gln	Asn	Thr	Phe	Tyr	Ala	Gly	Ala	Lys	Val		
			20					25					30				
Gly	Gln	Ser	Ser	Phe	His	His	Gly	Val	Asn	Gln	Leu	Lys	Ser	Gly	His		
		35					40					45					
Asp	Asp	Arg	Tyr	Asn	Asp	Lys	Thr	Arg	Lys	Tyr	Gly	Ile	Asn	Arg	Asn		
	50					55					60						
Ser	Val	Thr	Tyr	Gly	Val	Phe	Gly	Gly	Tyr	Gln	Ile	Leu	Asn	Gln	Asn		
65					70					75					80		
Asn	Phe	Gly	Leu	Ala	Ala	Glu	Leu	Gly	Tyr	Asp	Tyr	Tyr	Gly	Arg	Val		
				85					90					95			
Arg	Gly	Asn	Val	Asp	Glu	Phe	Arg	Thr	Val	Lys	His	Ser	Ala	His	Gly		
		100						105					110				
Leu	Asn	Leu	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp	Leu	Asp		
		115					120					125					
Val	Tyr	Gly	Lys	Val	Gly	Ile	Ala	Val	Val	Arg	Asn	Asp	Tyr	Lys	Lys		
	130					135					140						
Tyr	Gly	Ala	Glu	Asn	Thr	Asn	Glu	Ser	Thr	Thr	Lys	Phe	His	Lys	Leu		
145					150					155					160		
Lys	Ala	Ser	Thr	Ile	Leu	Gly	Ala	Gly	Val	Glu	Tyr	Ala	Ile	Leu	Pro		
				165					170					175			
Glu	Leu	Ala	Ala	Arg	Val	Glu	Tyr	Gln	Tyr	Leu	Asn	Lys	Ala	Gly	Asn		
		180						185					190				
Leu	Asn	Lys	Ala	Leu	Val	Arg	Ser	Gly	Thr	Gln	Asp	Val	Asp	Phe	Gln		
		195					200					205					
Tyr	Ala	Pro	Asp	Ile	His	Ser	Val	Thr	Ala	Gly	Leu	Ser	Tyr	Arg	Phe		
	210					215					220						
Gly	Gln	Gly	Ala	Val	Ala	Pro	Val	Val	Glu	Pro	Glu	Val	Val	Thr	Lys		
225					230					235					240		
Asn	Phe	Ala	Phe	Ser	Ser	Asp	Val	Leu	Phe	Asp	Phe	Gly	Lys	Ser	Ser		

245								250					255				
Leu	Lys	Pro	Ala	Ala	Ala	Thr	Ala	Leu	Asp	Ala	Ala	Asn	Thr	Glu	Ile		
			260					265					270				
Ala	Asn	Leu	Gly	Leu	Ala	Thr	Pro	Ala	Ile	Gln	Val	Asn	Gly	Tyr	Thr		
		275					280					285					
Asp	Arg	Ile	Gly	Lys	Glu	Ala	Ser	Asn	Leu	Lys	Leu	Ser	Gln	Arg	Arg		
	290					295					300						
Ala	Glu	Thr	Val	Ala	Asn	Tyr	Leu	Val	Ser	Lys	Gly	Gln	Asn	Pro	Ala		
305					310				315					320			
Asn	Val	Thr	Ala	Val	Gly	Tyr	Gly	Glu	Ala	Asn	Pro	Val	Thr	Gly	Ala		
			325					330						335			
Thr	Cys	Asp	Ala	Val	Lys	Gly	Arg	Lys	Ala	Leu	Ile	Ala	Cys	Leu	Ala		
		340					345						350				
Pro	Asp	Arg	Arg	Val	Glu	Val	Gln	Val	Gln	Gly	Ala	Lys	Asn	Val	Ala		
	355						360					365					

Met

<210> 154
 <211> 1076
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> pnp new

<220>
 <221> CDS
 <222> (1)..(1074)

<400> 154																
aat	att	aaa	gaa	ttc	gta	aaa	gaa	gcg	ggt	aaa	ccg	cgt	tgg	gat	tgg	48
Asn	Ile	Lys	Glu	Phe	Val	Lys	Glu	Ala	Gly	Lys	Pro	Arg	Trp	Asp	Trp	
1				5					10					15		
ggt gcg ccg gaa ccg aat acc gca tta atc aac caa gtt aaa gcg tta																96
Val	Ala	Pro	Glu	Pro	Asn	Thr	Ala	Leu	Ile	Asn	Gln	Val	Lys	Ala	Leu	
			20					25					30			
gcg gaa gcg cgt atc ggc gat gcg tat cgt att aca gaa aaa caa gcg																144
Ala	Glu	Ala	Arg	Ile	Gly	Asp	Ala	Tyr	Arg	Ile	Thr	Glu	Lys	Gln	Ala	
		35				40						45				
cgt tac gaa caa atc gat gca att aaa gcg gat gtt atc gca caa tta																192
Arg	Tyr	Glu	Gln	Ile	Asp	Ala	Ile	Lys	Ala	Asp	Val	Ile	Ala	Gln	Leu	
	50				55					60						
acc gca caa gac gaa acc gtt tct gaa ggt gcg att att gat att att																240
Thr	Ala	Gln	Asp	Glu	Thr	Val	Ser	Glu	Gly	Ala	Ile	Ile	Asp	Ile	Ile	
	65				70				75					80		
acc gca tta gaa agt tct att gtt cgc ggt cgt att att gcc ggc gaa																288
Thr	Ala	Leu	Glu	Ser	Ser	Ile	Val	Arg	Gly	Arg	Ile	Ile	Ala	Gly	Glu	
				85					90					95		

ccg	cgt	att	gac	ggg	cgt	acg	gta	gat	acg	gtt	cgt	gca	tta	gac	att	336
Pro	Arg	Ile	Asp	Gly	Arg	Thr	Val	Asp	Thr	Val	Arg	Ala	Leu	Asp	Ile	
			100					105					110			
tgc	acc	ggc	gta	tta	cct	cgt	acg	cac	ggg	tct	gca	atc	ttt	act	cgc	384
Cys	Thr	Gly	Val	Leu	Pro	Arg	Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg	
		115					120					125				
ggg	gaa	aca	caa	gca	tta	gcg	gtt	gca	acc	tta	ggg	act	gag	cgc	gat	432
Gly	Glu	Thr	Gln	Ala	Leu	Ala	Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	
	130					135					140					
gca	caa	att	gtt	gac	gaa	tta	acc	ggc	gag	aaa	tca	gac	cgt	ttc	tta	480
Ala	Gln	Ile	Val	Asp	Glu	Leu	Thr	Gly	Glu	Lys	Ser	Asp	Arg	Phe	Leu	
145						150				155					160	
ttc	cac	tat	aac	ttc	cct	ccg	tac	tct	gtc	ggg	gaa	acc	ggg	cgt	atc	528
Phe	His	Tyr	Asn	Phe	Pro	Pro	Tyr	Ser	Val	Gly	Glu	Thr	Gly	Arg	Ile	
				165					170					175		
ggg	tcg	ccg	aaa	cgt	cgt	gaa	atc	ggc	cac	ggg	cgt	tta	gcg	aaa	cgc	576
Gly	Ser	Pro	Lys	Arg	Arg	Glu	Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg	
			180					185					190			
ggg	gta	tta	gcg	gta	atg	ccg	act	gct	gaa	gaa	ttc	ccg	tat	gta	gtg	624
Gly	Val	Leu	Ala	Val	Met	Pro	Thr	Ala	Glu	Glu	Phe	Pro	Tyr	Val	Val	
		195					200					205				
cgc	gta	gta	tct	gaa	att	acc	gaa	tca	aac	ggg	tct	tct	tca	atg	gct	672
Arg	Val	Val	Ser	Glu	Ile	Thr	Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala	
	210					215					220					
tcc	gta	tgc	ggc	gca	tct	tta	gcg	tta	atg	gac	gca	ggc	gta	ccg	att	720
Ser	Val	Cys	Gly	Ala	Ser	Leu	Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile	
225						230				235					240	
aaa	gcg	gcg	gtt	gcg	ggg	atc	gca	atg	ggc	tta	gtg	aaa	gaa	gaa	gaa	768
Lys	Ala	Ala	Val	Ala	Gly	Ile	Ala	Met	Gly	Leu	Val	Lys	Glu	Glu	Glu	
				245					250					255		
aaa	ttt	gtg	gtg	ctt	tca	gac	atc	tta	ggg	gac	gaa	gac	cat	tta	ggc	816
Lys	Phe	Val	Val	Leu	Ser	Asp	Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly	
		260						265					270			
gat	atg	gac	ttc	aaa	gta	gcc	ggg	acg	cgt	gaa	ggg	gta	acc	gca	ctt	864
Asp	Met	Asp	Phe	Lys	Val	Ala	Gly	Thr	Arg	Glu	Gly	Val	Thr	Ala	Leu	
		275					280					285				
caa	atg	gat	att	aaa	atc	gaa	ggg	atc	acg	cct	gaa	att	atg	caa	atc	912
Gln	Met	Asp	Ile	Lys	Ile	Glu	Gly	Ile	Thr	Pro	Glu	Ile	Met	Gln	Ile	
	290					295					300					
gca	tta	aat	caa	gcg	aaa	ggg	gcg	cgt	atg	cac	atc	tta	agc	gtg	atg	960
Ala	Leu	Asn	Gln	Ala	Lys	Gly	Ala	Arg	Met	His	Ile	Leu	Ser	Val	Met	
305					310					315					320	
gaa	caa	gcg	att	cct	gca	cct	cgt	gcc	gat	att	tcc	gat	ttt	gcg	cct	1008
Glu	Gln	Ala	Ile	Pro	Ala	Pro	Arg	Ala	Asp	Ile	Ser	Asp	Phe	Ala	Pro	
				325				330						335		
cgt	att	cat	acg	atg	aag	atc	gat	ccg	aag	aaa	atc	aaa	gac	gtg	atc	1056
Arg	Ile	His	Thr	Met	Lys	Ile	Asp	Pro	Lys	Lys	Ile	Lys	Asp	Val	Ile	
			340					345					350			

ggt aaa ggc ggt gcg gtt at
Gly Lys Gly Gly Ala Val
355

<210> 155
<211> 358
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 155
Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
1 5 10 15
Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
20 25 30
Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
35 40 45
Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu
50 55 60
Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile
65 70 75 80
Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu
85 90 95
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
100 105 110
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
115 120 125
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp
130 135 140
Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
145 150 155 160
Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
165 170 175
Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
180 185 190
Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
195 200 205
Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
210 215 220
Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
225 230 235 240
Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu
245 250 255
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly
260 265 270
Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu

275		280		285
Gln Met Asp Ile Lys Ile	Glu Gly Ile Thr Pro	Glu Ile Met Gln Ile		
290	295	300		
Ala Leu Asn Gln Ala Lys	Gly Ala Arg Met His	Ile Leu Ser Val Met		
305	310	315		320
Glu Gln Ala Ile Pro Ala	Pro Arg Ala Asp Ile	Ser Asp Phe Ala Pro		
	325	330		335
Arg Ile His Thr Met Lys	Ile Asp Pro Lys Lys	Ile Lys Asp Val Ile		
	340	345		350
Gly Lys Gly Gly Ala Val				
355				

<210> 156
 <211> 1055
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> potD

<220>
 <221> CDS
 <222> (1)..(1053)

<400> 156	
atg aaa aaa tta gcg ggt tta ttt gca gca ggt tta gcg aca gtt gca	48
Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala	
1 5 10 15	
tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct	96
Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala	
20 25 30	
caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat	144
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr	
35 40 45	
gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa	192
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys	
50 55 60	
gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta	240
Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu	
65 70 75 80	
aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac	288
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn	
85 90 95	
tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat	336
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp	
100 105 110	
cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac	384
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn	
115 120 125	

aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly 130 135 140	432
gca ccg ggt atc gca ttt aac tca aat gac tat aag ggc gat gcg ttc Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe 145 150 155 160	480
act tct tgg ggt gat tta tgg aaa cct gag ttt gcg aat aaa gta caa Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln 165 170 175	528
tta tta gat gac gca cgt gaa gta ttt aac att gcg tta tta aaa tta Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu 180 185 190	576
ggt aaa aac cct aat aca acc aat ccg gaa gag att aaa gcg gct tac Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr 195 200 205	624
gaa gag tta aga aaa tta cgt cca aac gta ctt tct ttc act tca gac Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp 210 215 220	672
aac cca gcg aac tca ttt atc gca ggt gaa gta tct gta ggt caa tta Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu 225 230 235 240	720
tgg aac ggt tct gta cgt att gcg aaa aaa gaa caa gcg ccg gta aac Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn 245 250 255	768
atg gtg ttc cca aaa gaa ggt cct gta ctt tgg gtt gat acg tta gcc Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala 260 265 270	816
att ccg gcg aat gcg aaa aac aaa gaa aat gcg cat aag tta atc aac Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn 275 280 285	864
tac tta tta agc gca ccg gtt gcg gaa aaa tta acg tta gaa atc ggt Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly 290 295 300	912
tat ccg act tca aac gta gaa gcg tta aaa aca tta cca aaa gag att Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile 305 310 315 320	960
acc gaa gat ccg gca atc tat ccg aca gct gat gtg tta aaa gcg gca Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala 325 330 335	1008
caa tgg caa gac gat gta ggt aat gca atc gaa ctt tac gaa aaa ta Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys 340 345 350	1055

<210> 157

<211> 351

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 157

Met	Lys	Lys	Leu	Ala	Gly	Leu	Phe	Ala	Ala	Gly	Leu	Ala	Thr	Val	Ala	
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Leu	Thr	Ala	Cys	Asn	Glu	Glu	Lys	Pro	Lys	Ala	Ala	Glu	Ala	Ala	Ala	
			20					25					30			
Gln	Pro	Ala	Ala	Ala	Gly	Thr	Val	His	Leu	Tyr	Thr	Trp	Thr	Glu	Tyr	
		35					40					45				
Val	Pro	Glu	Gly	Leu	Leu	Asp	Glu	Phe	Thr	Lys	Gln	Thr	Gly	Ile	Lys	
	50					55					60					
Val	Glu	Val	Ser	Ser	Leu	Glu	Ser	Asn	Glu	Thr	Met	Tyr	Ala	Lys	Leu	
65					70					75					80	
Lys	Leu	Gln	Gly	Lys	Asp	Gly	Gly	Tyr	Asp	Val	Ile	Ala	Pro	Ser	Asn	
				85					90					95		
Tyr	Phe	Val	Ser	Lys	Met	Ala	Lys	Glu	Gly	Met	Leu	Ala	Glu	Leu	Asp	
			100					105					110			
His	Ala	Lys	Leu	Pro	Val	Ile	Lys	Glu	Leu	Asn	Gln	Asp	Trp	Leu	Asn	
		115					120					125				
Lys	Pro	Tyr	Asp	Gln	Gly	Asn	Lys	Tyr	Ser	Leu	Pro	Gln	Leu	Leu	Gly	
	130					135					140					
Ala	Pro	Gly	Ile	Ala	Phe	Asn	Ser	Asn	Asp	Tyr	Lys	Gly	Asp	Ala	Phe	
145					150					155					160	
Thr	Ser	Trp	Gly	Asp	Leu	Trp	Lys	Pro	Glu	Phe	Ala	Asn	Lys	Val	Gln	
			165						170					175		
Leu	Leu	Asp	Asp	Ala	Arg	Glu	Val	Phe	Asn	Ile	Ala	Leu	Leu	Lys	Leu	
		180						185					190			
Gly	Lys	Asn	Pro	Asn	Thr	Thr	Asn	Pro	Glu	Glu	Ile	Lys	Ala	Ala	Tyr	
		195					200					205				
Glu	Glu	Leu	Arg	Lys	Leu	Arg	Pro	Asn	Val	Leu	Ser	Phe	Thr	Ser	Asp	
	210					215					220					
Asn	Pro	Ala	Asn	Ser	Phe	Ile	Ala	Gly	Glu	Val	Ser	Val	Gly	Gln	Leu	
225					230					235					240	
Trp	Asn	Gly	Ser	Val	Arg	Ile	Ala	Lys	Lys	Glu	Gln	Ala	Pro	Val	Asn	
			245						250					255		
Met	Val	Phe	Pro	Lys	Glu	Gly	Pro	Val	Leu	Trp	Val	Asp	Thr	Leu	Ala	
			260					265					270			
Ile	Pro	Ala	Asn	Ala	Lys	Asn	Lys	Glu	Asn	Ala	His	Lys	Leu	Ile	Asn	
		275					280					285				
Tyr	Leu	Leu	Ser	Ala	Pro	Val	Ala	Glu	Lys	Leu	Thr	Leu	Glu	Ile	Gly	
	290					295					300					
Tyr	Pro	Thr	Ser	Asn	Val	Glu	Ala	Leu	Lys	Thr	Leu	Pro	Lys	Glu	Ile	
305					310					315					320	
Thr	Glu	Asp	Pro	Ala	Ile	Tyr	Pro	Thr	Ala	Asp	Val	Leu	Lys	Ala	Ala	
				325					330					335		

Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys
 340 345 350

<210> 158
 <211> 525
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> rpmF

<220>
 <221> CDS
 <222> (1)..(522)

<400> 158
 atg caa aag gta aaa cta ccc ctc acc att gac cca tat aaa gac gct 48
 Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala
 1 5 10 15
 cag cgt cga atg gat tac gaa ggc tac atc tca cgt agt ctg ctt aat 96
 Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn
 20 25 30
 cgt ttg ggt gaa tct gtg agc aat gtg cta agc gat gca caa gtt act 144
 Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr
 35 40 45
 ctc tcg tta tat atc gat ccg caa cgc tta acc gtt att aaa ggt acg 192
 Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr
 50 55 60
 gcg aca gtg gaa gtg gaa ttc gat tgc caa cga tgc ggt aac ccg ttt 240
 Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
 65 70 75 80
 aca caa acg ctt gac tgt tcg ttt tgt ttc agt ccg gtg tcc aat atg 288
 Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
 85 90 95
 gat cag gcg gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac 336
 Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
 100 105 110
 gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc 384
 Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
 115 120 125
 atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgt gaa gtg 432
 Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
 130 135 140
 tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa 480
 Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
 145 150 155 160
 aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag 525
 Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
 165 170

<210> 159

<211> 174

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 159

Met	Gln	Lys	Val	Lys	Leu	Pro	Leu	Thr	Ile	Asp	Pro	Tyr	Lys	Asp	Ala	
1				5					10					15		
Gln	Arg	Arg	Met	Asp	Tyr	Glu	Gly	Tyr	Ile	Ser	Arg	Ser	Leu	Leu	Asn	
			20					25					30			
Arg	Leu	Gly	Glu	Ser	Val	Ser	Asn	Val	Leu	Ser	Asp	Ala	Gln	Val	Thr	
		35					40					45				
Leu	Ser	Leu	Tyr	Ile	Asp	Pro	Gln	Arg	Leu	Thr	Val	Ile	Lys	Gly	Thr	
	50					55					60					
Ala	Thr	Val	Glu	Val	Glu	Phe	Asp	Cys	Gln	Arg	Cys	Gly	Asn	Pro	Phe	
65					70				75						80	
Thr	Gln	Thr	Leu	Asp	Cys	Ser	Phe	Cys	Phe	Ser	Pro	Val	Ser	Asn	Met	
				85					90					95		
Asp	Gln	Ala	Asp	Asn	Leu	Pro	Glu	Ile	Tyr	Glu	Pro	Ile	Glu	Val	Asn	
			100					105					110			
Glu	Phe	Gly	Glu	Val	Asn	Leu	Leu	Asp	Met	Ile	Glu	Asp	Gly	Phe	Ile	
		115					120					125				
Ile	Glu	Leu	Pro	Leu	Val	Pro	Met	His	Ser	Glu	Glu	His	Cys	Glu	Val	
	130					135					140					
Ser	Val	Ser	Glu	Gln	Val	Phe	Gly	Glu	Leu	Pro	Glu	Glu	Leu	Ala	Lys	
145					150					155					160	
Lys	Pro	Asn	Pro	Phe	Ala	Val	Leu	Ala	Asn	Leu	Lys	Lys	Asn			
				165					170							

<210> 160

<211> 1302

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> tig

<220>

<221> CDS

<222> (1)..(1299)

<400> 160

atg	tca	att	tct	att	gaa	act	tta	gaa	ggc	tta	caa	cgc	cgc	gta	act	48
Met	Ser	Ile	Ser	Ile	Glu	Thr	Leu	Glu	Gly	Leu	Gln	Arg	Arg	Val	Thr	
1				5					10					15		
att	acc	gta	gct	gct	gat	aaa	atc	gaa	gcg	gct	tac	aaa	gag	caa	tta	96
Ile	Thr	Val	Ala	Ala	Asp	Lys	Ile	Glu	Ala	Ala	Tyr	Lys	Glu	Gln	Leu	
			20					25					30			
aaa	ggc	tat	gcg	aaa	aac	gct	cgt	gta	gac	ggt	ttc	cgt	aaa	ggt	aaa	144
Lys	Gly	Tyr	Ala	Lys	Asn	Ala	Arg	Val	Asp	Gly	Phe	Arg	Lys	Gly	Lys	
		35					40					45				

gta	ccg	cac	gca	att	atc	gaa	caa	cgt	ttc	ggg	tta	gcg	gct	cgc	caa	192
Val	Pro	His	Ala	Ile	Ile	Glu	Gln	Arg	Phe	Gly	Leu	Ala	Ala	Arg	Gln	
	50					55					60					
gac	gta	tta	tcc	gat	gaa	atg	caa	cgt	gcg	ttc	ttt	gat	gcg	gta	atc	240
Asp	Val	Leu	Ser	Asp	Glu	Met	Gln	Arg	Ala	Phe	Phe	Asp	Ala	Val	Ile	
65					70					75					80	
gct	gag	aaa	att	aac	ctt	gcc	ggg	cgt	cct	acc	ttc	aca	ccg	aac	aac	288
Ala	Glu	Lys	Ile	Asn	Leu	Ala	Gly	Arg	Pro	Thr	Phe	Thr	Pro	Asn	Asn	
				85					90					95		
tac	caa	ccg	agt	caa	gaa	ttc	agc	ttc	act	gca	act	ttt	gaa	gta	ttc	336
Tyr	Gln	Pro	Ser	Gln	Glu	Phe	Ser	Phe	Thr	Ala	Thr	Phe	Glu	Val	Phe	
			100					105					110			
ccg	gaa	gtt	gaa	tta	aaa	ggc	tta	gaa	aat	atc	gaa	gtt	gaa	aaa	ccg	384
Pro	Glu	Val	Glu	Leu	Lys	Gly	Leu	Glu	Asn	Ile	Glu	Val	Glu	Lys	Pro	
	115						120					125				
gtt	gta	gaa	atc	aca	gaa	gct	gat	tta	gac	aaa	atg	atc	gat	gtg	tta	432
Val	Val	Glu	Ile	Thr	Glu	Ala	Asp	Leu	Asp	Lys	Met	Ile	Asp	Val	Leu	
	130					135					140					
cgt	aaa	caa	caa	gcg	act	tgg	gct	gaa	tct	caa	gca	gcg	gca	caa	gcg	480
Arg	Lys	Gln	Gln	Ala	Thr	Trp	Ala	Glu	Ser	Gln	Ala	Ala	Ala	Gln	Ala	
145					150					155					160	
gaa	gac	cgt	gtt	gta	atc	gac	ttc	gta	ggg	tct	gta	gac	ggg	gaa	gag	528
Glu	Asp	Arg	Val	Val	Ile	Asp	Phe	Val	Gly	Ser	Val	Asp	Gly	Glu	Glu	
				165					170					175		
ttt	gaa	ggc	ggg	aaa	gcg	aca	gac	ttc	act	tta	gca	atg	ggg	caa	agt	576
Phe	Glu	Gly	Gly	Lys	Ala	Thr	Asp	Phe	Thr	Leu	Ala	Met	Gly	Gln	Ser	
			180					185					190			
cgt	atg	atc	cct	ggg	ttt	gaa	gaa	ggg	atc	gtt	ggg	cac	aaa	gcc	ggc	624
Arg	Met	Ile	Pro	Gly	Phe	Glu	Glu	Gly	Ile	Val	Gly	His	Lys	Ala	Gly	
		195					200					205				
gaa	caa	ttc	gat	atc	gat	gtt	act	ttc	cct	gaa	gaa	tac	cac	gct	gaa	672
Glu	Gln	Phe	Asp	Ile	Asp	Val	Thr	Phe	Pro	Glu	Glu	Tyr	His	Ala	Glu	
	210					215					220					
aac	tta	aaa	ggg	aaa	gcg	gcg	aaa	ttc	gca	att	aca	ctt	aag	aaa	gta	720
Asn	Leu	Lys	Gly	Lys	Ala	Ala	Lys	Phe	Ala	Ile	Thr	Leu	Lys	Lys	Val	
225					230					235					240	
gaa	aat	atc	gta	tta	cct	gaa	tta	acc	gaa	gaa	ttc	gtg	aaa	aaa	ttc	768
Glu	Asn	Ile	Val	Leu	Pro	Glu	Leu	Thr	Glu	Glu	Phe	Val	Lys	Lys	Phe	
				245					250					255		
ggg	tca	gca	aaa	act	gta	gaa	gat	tta	cgt	gcg	gaa	att	aag	aaa	aat	816
Gly	Ser	Ala	Lys	Thr	Val	Glu	Asp	Leu	Arg	Ala	Glu	Ile	Lys	Lys	Asn	
			260					265					270			
atg	caa	cgt	gaa	ctt	aaa	aac	gca	gta	acc	gca	cgc	gtt	aaa	aac	caa	864
Met	Gln	Arg	Glu	Leu	Lys	Asn	Ala	Val	Thr	Ala	Arg	Val	Lys	Asn	Gln	
		275					280					285				
gta	atc	aac	ggg	tta	atc	gca	caa	aat	gaa	att	gaa	gtg	ccg	gct	gca	912
Val	Ile	Asn	Gly	Leu	Ile	Ala	Gln	Asn	Glu	Ile	Glu	Val	Pro	Ala	Ala	
	290					295					300					

gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt	960
Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg	
305 310 315 320	
ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc	1008
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe	
325 330 335	
gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc	1056
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr	
340 345 350	
gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa	1104
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu	
355 360 365	
acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt	1152
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val	
370 375 380	
gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta	1200
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val	
385 390 395 400	
gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta	1248
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val	
405 410 415	
act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa	1296
Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln	
420 425 430	
ggc taa	1302
Gly	

<210> 161
 <211> 433
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 161
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 Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
 20 25 30
 Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
 35 40 45
 Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
 50 55 60
 Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
 65 70 75 80
 Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
 85 90 95
 Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
 100 105 110

Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
115 120 125

Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
130 135 140

Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
145 150 155 160

Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
165 170 175

Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
180 185 190

Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly
195 200 205

Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
210 215 220

Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
225 230 235 240

Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
245 250 255

Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
260 265 270

Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
275 280 285

Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
290 295 300

Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
305 310 315 320

Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
325 330 335

Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
340 345 350

Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
355 360 365

Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
370 375 380

Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
385 390 395 400

Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
405 410 415

Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
420 425 430

Gly

<210> 162
<211> 316
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> tRNA-glu

<400> 162
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ggcctaggac atcgcccttt cacggcggtta accgggggttc gaatccccgt ggggacgcca 120
tttaaagatg acttttgttg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180
tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
agctgaacaa aagcagctaa gtgttttagtt gaataaagta tcgcgttgaa tgcgttcaaa 300
taaaatttga aaatat 316

<210> 163
<211> 85
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> tRNA-leu

<400> 163
gctctggtgg tggaattggt agacacgcta tcttgagggg gtagtgtcca taggatgtgc 60
gagttcgagt ctgcccaga gcacc 85

<210> 164
<211> 623
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> yaeE

<220>
<221> CDS
<222> (1)..(621)

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Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr
1 5 10 15
ctt gaa acg ctc tat atg ggc ttt gcg gcg act tta ctt gct gtg gta 96
Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val
20 25 30
gtc ggt ttg ccg atc ggt ttt ctg gca ttt tta acc ggt aaa gga gag 144
Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu
35 40 45
att tta gag aat ccg cgt tta cat caa gta tta gat gtg att att aat 192
Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn

50	55	60	
atc ggt cgt tcc gta ccg ttt att att ttg tta gtc gtg ttg tta cct Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro 65 70 75 80			240
ttt acg cgt tta ttg gtc ggg aca acg ctc ggt act acg gcg gcg att Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile 85 90 95			288
gtg ccg tta agc gtt tcg gca att ccg ttt ttt gcg cgt tta act tca Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser 100 105 110			336
aat gcg tta tta gaa atc cca gca ggt tta acc gaa gcg gcg aaa tcg Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser 115 120 125			384
atg ggc gca acg aat tgg caa gtg gtc agt aaa ttt tat tta ccg gaa Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu 130 135 140			432
tca ctg ccg att tta atc aat ggt atc aca tta act tta gtc gct tta Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu 145 150 155 160			480
atc ggt tat tcg gca atg gcg ggt gcg gtc ggc ggc ggc ggt ttg ggt Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly 165 170 175			528
aac ctt gcc atc agt tac ggt gaa cac cga aat atg gtc tat gta aaa Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys 180 185 190			576
tgg atc tca aca att att atc gta gcg att gtg atg atc agt caa aa Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln 195 200 205			623

<210> 165

<211> 207

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 165

Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr
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Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val
20 25 30

Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu
35 40 45

Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn
50 55 60

Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro
65 70 75 80

Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile
85 90 95

- 255 -

Val	Pro	Leu	Ser	Val	Ser	Ala	Ile	Pro	Phe	Phe	Ala	Arg	Leu	Thr	Ser
			100					105					110		
Asn	Ala	Leu	Leu	Glu	Ile	Pro	Ala	Gly	Leu	Thr	Glu	Ala	Ala	Lys	Ser
		115					120					125			
Met	Gly	Ala	Thr	Asn	Trp	Gln	Val	Val	Ser	Lys	Phe	Tyr	Leu	Pro	Glu
	130					135					140				
Ser	Leu	Pro	Ile	Leu	Ile	Asn	Gly	Ile	Thr	Leu	Thr	Leu	Val	Ala	Leu
145					150					155					160
Ile	Gly	Tyr	Ser	Ala	Met	Ala	Gly	Ala	Val	Gly	Gly	Gly	Gly	Leu	Gly
				165					170					175	
Asn	Leu	Ala	Ile	Ser	Tyr	Gly	Glu	His	Arg	Asn	Met	Val	Tyr	Val	Lys
			180					185					190		
Trp	Ile	Ser	Thr	Ile	Ile	Ile	Val	Ala	Ile	Val	Met	Ile	Ser	Gln	
		195					200					205			